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<b>(21) International Application Number:</b> PCT/EP99/05652 <b>(22) International Filing Date:</b> 4 August 1999 (04.08.99) <b>(30) Priority Data:</b> 98202634.6 4 August 1998 (04.08.98) EP <b>(71) Applicant (for all designated States except US):</b> VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE [BE/BE]; Rijvisschestraat 120, B-9052 Zwijnaarde (BE). <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> LEE, Jeong, Hee [KR/BE]; Spinnmolenplein 274 (22K), B-9000 Gent (BE). VERBRUGGEN, Nathalie [BE/BE]; Avenue des Saisons, 53, B-1050 Ixelles (BE). <b>(74) Agent:</b> DE CLERCQ, Ann; Ann De Clercq & Co. B.V.B.A., Brandstraat 100, B-9830 Sint-Martens-Latem (BE).		<b>(81) Designated States:</b> AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
<b>(54) Title:</b> GENES INVOLVED IN TOLERANCE TO ENVIRONMENTAL STRESS		
<b>(57) Abstract</b>  <p>The present invention relates to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress resistance in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells. The present invention further relates to an isolated polynucleic acid obtainable by such a method as listed in Table 1 as well as recombinant polynucleic acid comprising the same. The present invention further relates to an isolated polypeptide encoded by a polynucleic acid of the invention. The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into a plant cell a recombinant DNA comprising a polynucleic acid as defined which when expressed in a plant cell enhances the tolerances or induces resistance to environmental stress conditions of said plant. The present invention particularly relates to plant cells, plants or harvestable parts or propagation material thereof transformed with a recombinant polynucleic acid as defined above.</p>		

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**Genes Involved in tolerance to environmental stress**

The present invention relates to molecular biology, in particular plant  
5 molecular biology. In particular, the invention relates to improvements of crop  
productivity of useful plants. One of the major limitations of crop productivity is the  
effect of environmental stress conditions on plant growth and development. An  
important goal of molecular biology is the identification and isolation of genes that can  
provide resistance or tolerance to such stresses. For agriculture, the creation of  
10 transgenic plants containing such genes provides the potential for improving the stress  
resistance or tolerance of plants.

Drought, salt loading, and freezing are stresses that cause adverse effects on  
the growth of plants and the productivity of crops. The physiological response to these  
stresses arises out of changes in cellular gene expression. Expression of a number of  
15 genes has been demonstrated to be induced by these stresses (Zhu et al., 1997;  
Shinozaki et al., 1996; Thomashow, 1994). The products of these genes can be  
classified into two groups: those that directly protect against environmental stresses  
and those that regulate gene expression and signal transduction in the stress  
response. The first group includes proteins that likely function by protecting cells from  
20 dehydration, such as the enzymes required for biosynthesis of various  
osmoprotectants, late-embryogenesis-abundant (LEA) proteins, antifreeze proteins,  
chaperones, and detoxification enzymes (Shinozaki et al., 1997, Ingram et al., 1996,  
Bray et al., 1997). The second group of gene products includes transcription factors,  
protein kinases, and enzymes involved in phosphoinositide metabolism (Shinozaki et  
25 al., 1997). An overview of the methods known to improve stress tolerance in plants is  
also given in Holmberg & Bülow, (1998).

Further studies are definitely needed to give an insight into the mechanisms  
involved in the plant response to environmental stress conditions.

The study of plants naturally adapted to extreme desiccation has led to the  
30 hypothesis that the genetic information for tolerance to environmental stress conditions  
exists in all higher plants. In glycophytes, this information would only be expressed in  
seeds and pollen grains which undergo a desiccation process.

The induction of osmotolerance in plants is very important to crop productivity:  
30 to 50 % of the land under irrigation is presently affected by salinity. Several lines of  
35 evidence also demonstrate that even mild environmental stress conditions throughout  
the growth season have a negative impact on plant growth and crop productivity. It is

for instance known that even minor limitations in water availability cause a reduced photosynthetic rate. Unpredictable rainfall, increase in soil salinity at the beginning and the end of the growing season often result in decreased plant growth and crop productivity. These environmental factors share at least one element of stress and that is water deficit or dehydration. Drought is a significant problem in agriculture today. Over the last 40 years, for example, drought accounted for 74% of the total US crop losses of corn. To sustain productivity under adverse environmental conditions, it is important to provide crops with a genetic basis for coping with water deficit, for example by breeding water retention and tolerance mechanisms into crops so that they can grow and yield under these adverse conditions.

It is an aim of the present invention to provide a new method for screening for plant genes involved in tolerance or resistance to environmental stress.

It is an aim of the present invention to provide new plant genes, more particularly plant genes providing the potential of improving the tolerance to environmental stress conditions in plants.

It is also an aim of the present invention to provide polypeptides encoded by said new plant genes.

It is further an aim of the present invention to provide methods for producing plants with enhanced tolerance or resistance to environmental stress conditions based on said new genes.

It is also an aim of the present invention to provide recombinant polynucleic acids comprising said new genes.

It is further an aim of the present invention to provide plant cells and plants transformed with said new genes.

It is further an aim of the present invention to provide plant cells and plants with enhanced tolerance or resistance to environmental stress conditions.

The present invention relates more particularly to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

It has been found that the transfer of genes from plants which are often difficult to assay for certain characteristics, to lower eukaryotes, such as yeasts and fungi, but

in particular yeast, especially *Saccharomyces*, is relatively-easy to achieve, whereby it has now been shown that the results of testing for tolerance or resistance to environmental conditions in the resulting yeast cells gives a relatively reliable measure of the capability of the inserted coding sequence or gene to induce tolerance or resistance to environmental stress in plants. Thus the expression of polynucleic acid sequences comprising the gene or coding sequence which are responsible for inducing tolerance or resistance to environmental stress conditions can be enhanced in the plant species from which it originates or in any other plant species.

In the present context the term "enhancing" must be understood to mean that the levels of molecules correlated with stress protection in a transformed plant cell, plant tissue or plant part will be "substantially increased" or "elevated" meaning that this level will be greater than the levels in an untransformed plant.

This may be achieved by inducing overexpression of suitable genetic information which is already present, or by any other suitable means of introducing into the plant cell heterologous information resulting in a capability to tolerate or resist environmental stress.

The term "environmental stress" has been defined in different ways in the prior art and largely overlaps with the term "osmotic stress". Holmberg et al., 1998 for instance define different environmental stress factors which result in abiotic stress. Salinity, drought, heat, chilling and freezing are all described as examples of conditions which induce osmotic stress. The term "environmental stress" as used in the present invention refers to any adverse effect on metabolism, growth or viability of the cell, tissue, seed, organ or whole plant which is produced by an non-living or non-biological environmental stressor. More particularly, it also encompasses environmental factors such as water stress (flooding, drought, dehydration), anaerobic (low level of oxygen, CO<sub>2</sub> etc.), aerobic stress, osmotic stress, salt stress, temperature stress (hot/heat, cold, freezing, frost) or nutrients/pollutants stress.

The term "anaerobic stress" means any reduction in oxygen levels sufficient to produce a stress as hereinbefore defined, including hypoxia and anoxia.

The term "flooding stress" refers to any stress which is associated with or induced by prolonged or transient immersion of a plant, plant part, tissue or isolated cell in a liquid medium such as occurs during monsoon, wet season, flash flooding or excessive irrigation of plants, etc.

"Cold stress" and "heat stress" are stresses induced by temperatures which are respectively, below or above, the optimum range of growth temperatures for a

particular plant species. Such optimum growth temperature ranges are readily determined or known to those skilled in the art.

“Dehydration stress” is any stress which is associated with or induced by the loss of water, reduced turgor or reduced water content of a cell, tissue, organ or whole  
5 plant.

“Drought stress” refers to any stress which is induced by or associated with the deprivation of water or reduced supply of water to a cell, tissue, organ or organism.

“Oxidative stress” refers to any stress which increases the intracellular level of reactive oxygen species.

10 The terms “salinity-induced stress”, “salt-stress” or similar term refer to any stress which is associated with or induced by elevated concentrations of salt and which result in a perturbation in the osmotic potential of the intracellular or extracellular environment of a cell.

Said salt can be for example, water soluble inorganic salts such as sodium  
15 sulfate, magnesium sulfate, calcium sulfate, sodium chloride, magnesium chloride, calcium chloride, potassium chloride etc., salts of agricultural fertilizers and salts associated with alkaline or acid soil conditions.

The transgenic plants obtained in accordance with the method of the present invention, upon the presence of the polynucleic acid and/or regulatory sequence  
20 introduced into said plant, attain resistance, tolerance or improved tolerance or resistance against environmental stress which the corresponding wild-type plant was susceptible to.

The terms “tolerance” and “resistance” cover the range of protection from a delay to complete inhibition of alteration in cellular metabolism, reduced cell growth  
25 and/or cell death caused by the environmental stress conditions defined herein before. Preferably, the transgenic plant obtained in accordance with the method of the present invention is tolerant or resistant to environmental stress conditions in the sense that said plant is capable of growing substantially normal under environmental conditions where the corresponding wild-type plant shows reduced growth, metabolism, viability,  
30 productivity and/or male or female sterility. Methodologies to determine plant growth or response to stress include, but are not limited to height measurements, leaf area, plant water relations, ability to flower, ability to generate progeny and yield or any other methodology known to those skilled in the art.

The terms “tolerance” and “resistance” may be used interchangeably in the  
35 present invention.

The methods according to the invention as set out below can be applied to any, higher plant, preferably important crops, preferably to all cells of a plant leading to an enhanced osmotic or any other form of environmental stress tolerance. By means of the embodiments as set out below, it now becomes possible to grow crops with improved yield, growth, development and productivity under environmental stress conditions, it may even become possible for instance to grow crops in areas where they cannot grow without the induced osmotolerance according to the invention.

In order to do a thorough screening for relevant plant genes and/or coding sequences, it is preferred to apply a method according to the invention whereby said cDNA library comprises copies of essentially all mRNA of said plant cell. Probably only coding sequences are sufficient. For the screening of genes involved in environmental stress, it is preferred to use a cDNA library from siliques (fruits, containing the maturing seeds), such as the siliques from *Arabidopsis*, because genes involved in for instance osmotolerance are preferentially expressed in these organs.

Although the genetic information may be introduced into yeast for screening by any suitable method, as long as it is in a functional format long enough for testing of tolerance or resistance to environmental stress conditions, it is preferred for ease of operation to use a well known vector such as a 2 $\mu$  plasmid. It is to be preferred to have the coding sequence or the gene under control of a strong constitutive yeast promoter, to enhance good expression of the gene or coding sequence of interest. Strong constitutive yeast promoters are well known in the art and include, but are not limited to the yeast TPI promoter.

The term "gene" as used herein refers to any DNA sequence comprising several operably linked DNA fragments such as a promoter and a 5' untranslated region (the 5'UTR), a coding region (which may or may not code for a protein), and an untranslated 3' region (3'UTR) comprising a polyadenylation site. Typically in plant cells, the 5'UTR, the coding region and the 3'UTR (together referred to as the transcribed DNA region) are transcribed into an RNA which, in the case of a protein encoding gene, is translated into a protein. A gene may include additional DNA fragments such as, for example, introns. As used herein, a genetic locus is the position of a given gene in the genome of a plant.

The present invention more particularly relates to an isolated polynucleic acid obtainable by a method comprising the preparation of a cDNA as set out above comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an

enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

The term "polynucleic acid" refers to DNA or RNA, or amplified versions thereof, or the complement thereof.

5       The present invention more particularly provides an isolated polynucleic acid obtainable by a method as defined above which encodes a polypeptide as listed in Table 1.

10       The capacity of an isolated polynucleic acid to confer tolerance or resistance to environmental stress conditions can be tested according to methods well-known in the art, see for example, Grillo et al. (1996), Peassarakli et al. (Editor), Nilsen et al. (1996), Shinozaki et al. (1999), Jones et al. (1989), Fowden et al. (1993) or as described in the appended examples.

15       The present invention more particularly relates to an isolated polynucleic acid which encodes a homolog of any of the polypeptides as listed in Table 1, which is chosen from:

- (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, or 121, or the complementary strands thereof;
- 20       (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- 25       (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

30       Said fragment as defined above are preferably unique fragments of said sequences.

The term "hybridizing" refers to hybridization conditions as described in Sambrook (1989), preferably specific or stringent hybridization conditions are aimed at.

Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T<sub>m</sub>) for the specific sequence at a defined ionic strength and pH. The T<sub>m</sub> is the temperature (under defined ionic strength and pH) at which  
5 50% of the target sequence hybridizes to a perfectly matched probe. Typically, stringent conditions will be those in which the salt concentration is about 0.02 molar at pH 7 and the temperature is at least about 60°C.

In the present invention, genomic DNA or cDNA comprising the polynucleic acids of the invention can be identified in standard Southern blots under stringent  
10 conditions using the cDNA sequence shown. The preparation of both genomic and cDNA libraries is within the skill of the art. Examples of hybridization conditions are also given in the Examples section.

The present invention also relates to the isolated polynucleic acids which encode polypeptides which are a homolog of the polypeptides as set out in Table 1  
15 useful for the production of plants which are resistant or tolerant to environmental stress conditions.

The present invention also relates to a polynucleic acid comprising at least part of any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or  
20 at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121. Preferably, said gene encodes a protein having  
25 substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76 or 78. Said part of said gene is preferably a unique part.

The present invention preferably relates to the use of a polynucleic acid comprising at least part of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25,  
30 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%,  
35 80% or 85% identical, and most preferably at least 90% or 95% identical to any of

SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121 for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

The present invention particularly relates to an isolated polynucleic acid as defined above, which encodes a plant homolog of yeast DBF2 kinase, more particularly a DBF2 kinase homolog from *Arabidopsis thaliana* termed At-DBF2, which can at least be used to confer enhanced environmental stress tolerance or resistance in plants and yeast.

More preferably, the present invention relates to an isolated polynucleic acid encoding a plant DFB2 kinase, which is chosen from:

- (a) SEQ ID NO 1, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

Alternatively, the present invention relates to a polynucleic acid derived from a plant comprising at least part of SEQ ID NO 1, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 1. Preferably said gene encodes a protein

having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2.

The present invention also relates to the use of an isolated polynucleic acid as defined above which encodes a plant HSP 17.6A protein for the production of transgenic plants, more particularly a homolog from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- 10 (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 15 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to the use of a polynucleic acid comprising at least part of SEQ ID NO 3, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 3. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 4, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;

- 5 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

10 for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

The present invention preferably relates to the use of a polynucleic acid comprising at least part of any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more

15 preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

20 Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

According to another preferred embodiment, the present invention relates to an isolated polynucleic acid as defined above, which encodes a protein termed c74,

25 more particularly a plant homolog of c74, even more preferably a c74 from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More particularly, the present invention relates to an isolated polynucleic acid as defined above, which is chosen from:

30

- (a) SEQ ID NO 5, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 5 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

10 The present invention also relates to a polynucleic acid comprising at least part of SEQ ID NO 5, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 5. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 6.

15 Two nucleic acid sequences or polypeptides are said to be "identical" according to the present invention if the sequence of nucleotides or amino acid residues, respectively, in the two sequences is the same when aligned for maximum correspondence as described below. The term "complementary to" is used herein to mean that the complementary sequence hybridizes to all or a portion of a given polynucleotide sequence.

20 Sequence comparisons between two (or more) polynucleic acid or polypeptide sequences are typically performed by comparing sequences of the two sequences over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window", as used herein, refers to a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

30 Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (1981), by the homology alignment algorithm of Needleman and Wunsch (1970), by the search for similarity method of Pearson and Lipman (1988), by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by visual inspection.

"Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleic acid or polypeptide sequences in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not  
5 comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the  
10 percentage of sequence identity.

The term "substantial identity" of polynucleic acid or polypeptide sequences means that a polynucleotide sequence comprises a sequence that has at least 60%, 65%, 70% or 75% sequence identity, preferably at least 80% or 85%, more preferably at least 90% and most preferably at least 95 %, compared to a reference sequence  
15 using the programs described above (preferably BLAST) using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means  
20 sequence identity of at least 40%, 45%, 50% or 55% preferably at least 60%, 65%, 70%, 75%, 80% or 85% more preferably at least 90%, and most preferably at least 95%. Polypeptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes. Conservative amino acid substitutions refer to the interchangeability of  
25 residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and  
30 tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other, or a third nucleic acid, under stringent conditions.

More particularly, the polynucleic acids as used herein will comprise at least part of a DNA sequence which is essentially similar, or, preferentially, essentially  
5 identical or identical to one or both of the nucleotide or amino acid sequences corresponding to SEQ ID NO 1 to 121 disclosed herein, more specifically in the nucleotide sequence encoding, or the amino-acid sequence corresponding to the "active domain" of the respective protein or polypeptide.

The polynucleic acid sequences according to the present invention can be  
10 produced by means of any nucleic acid amplification technique known in the art such as PCR or conventional chemical synthesis.

For a general overview of PCR see PCR Protocols (Innis et al. (1990)).

Polynucleotides may also be synthesized by well-known techniques as described in the technical literature. See, e.g., Carruthers et al. (1982) and Adams et  
15 al. (1983). Double stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

The present invention more particularly relates to an isolated polypeptide  
20 encoded by a polynucleic acid according to any of the polynucleic acids as defined above, or a functional fragment thereof.

The present invention preferably relates to an isolated polypeptide as listed in Table 1 or to an isolated polypeptide encoded by a polynucleic acid isolated as defined above. Preferably, the present invention relates to polypeptides or peptides having at  
25 least part of the sequence of any of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Preferably, said part is a unique part and preferably includes the active domain of said polypeptide. Preferably said polypeptide is a  
30 recombinant polypeptide.

The term "isolated" distinguishes the protein or polynucleic acid according to the invention from the naturally occurring one.

The present invention also relates to a polypeptide comprising at least part of a polypeptide which is at least 50%, 55%, 60%, 65% identical, preferentially at least  
35 70%, 75% identical, more preferably at least 80% or 85% identical, and most

preferably at least 90% or 95% identical to any of SEQ ID NO NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120.

5           The terms "polypeptide" and "protein" are used interchangeably throughout the present description.

Said polypeptide preferably has the ability to confer tolerance or resistance to environmental stress conditions in at least plants, plant parts, plant tissues, plant cells, plant calli or yeast.

10           The term "functional fragment" refers to a fragment having substantially the biological activity of the protein from which it is derived.

The polypeptides of the present invention may be produced by recombinant expression in prokaryotic and eukaryotic engineered cells such as bacteria, yeast or fungi. It is expected that those of skill in the art are knowledgeable in the numerous  
15 expression systems available for expression in these systems.

The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell  
20 enhances tolerance or resistance to environmental stress of said plant.

The term "plant cell" as defined above also comprises plant tissue or a plant as a whole. The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any  
25 of the polynucleic acids encoding a protein as listed in Table 1 which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress in said plant.

The term "(over)expression" refers to the fact that the polypeptides of the invention encoded by said polynucleic acid are preferably expressed in an amount  
30 effective to confer tolerance or resistance to the transformed plant, to an amount of salt, heat, cold, (or other stress factors) that inhibits the growth of the corresponding untransformed plant.

Several methods to obtain transient introduction and expression of a recombinant DNA in a plant are known to the art. For example, plant virus vectors can

be used to obtain such purpose. Examples conferring to the use of plant viral vectors are described in Porta and Lomonossoff (1996), WO9320217 and US 5,589,367.

The present invention also relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising stably  
5 introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances the environmental stress tolerance or resistance of a plant.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method  
10 comprising introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed Table 1 which when (over)expressed in a plant cell enhances the environmental stress resistance of said plant.

According to a preferred embodiment, the present invention relates to a  
15 method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a DBF2 kinase, preferably a plant DBF2 kinase, most preferably an Arabidopsis DBF2 kinase.

According to another preferred embodiment, the present invention relates to a  
20 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding an HSP 17.6A protein, preferably a plant HSP 17.6A protein, most preferably an Arabidopsis HSP 17.6A.

According to a preferred embodiment, the present invention relates to a  
25 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a c74 protein, preferably a plant c74 protein, most preferably a Arabidopsis c74 protein.

Preferably, the present invention relates to a method as defined above,  
30 comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a polynucleic acid as defined above, and,
- a plant expressible promoter, whereby said  
35 polynucleic acid is in the same transcriptional unit

and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising indirectly increasing of inducing the expression of an endogenous gene in said plant comprised within a polynucleic acid as defined above or indirectly increasing of inducing the activity of a protein as defined above.

The present invention also relates to a method as defined above, comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid or indirectly increases or induces the protein activity of a protein encoded by said polynucleic acid of the present invention, and,
- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

A "recombinant" DNA molecule will comprise a "heterologous sequence" meaning that said recombinant DNA molecule will comprise a sequence originating from a foreign species, or, if from the same species, may be substantially modified from its original form. For example, a promoter operably linked to a structural gene which is from a species different from which the structural gene was derived, or, if from the same species, may be substantially modified from its original form.

The present invention also relates to a method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method comprising indirectly increasing or inducing the expression of an endogenous gene in said plant comprised within a polynucleic acid as defined above or indirectly increasing or inducing the activity of a protein of the invention as defined above. According to this embodiment, other polynucleic acids modulating the expression or the activity of a protein according to the present invention may be introduced

transiently or stably into the genome of said plants. The term "modulating" means enhancing, inducing, increasing, decreasing or inhibiting.

Increase or induction of expression or induction or increase of protein activity is required when said regulator protein is a positive regulator of the expression or the activity of at least one of the polynucleic acids or protein of the present invention.

Decrease or inhibition of expression or decrease or inhibition of protein activity is required when said regulator protein is a negative regulator of the expression or activity of at least one of the polynucleic acids or proteins of the present invention.

Increase of the activity of said polypeptide according to the present invention is obtained, according to one embodiment of the invention, by influencing endogenous gene expression in the plant. This is preferably achieved by the introduction of one or more polynucleic acid sequences according to the invention into the plant genome, in a suitable conformation for gene expression (e.g. under control of a plant-expressible promoter). This will result in increased or induced expression (overexpression) or increased or induced activity of the protein in the plant cells, and, in the presence of an adequate substrate, in an increase of tolerance or resistance to environmental stress conditions in a transgenic plant or plant cell as compared to a non-transgenic plant or plant cell. This increase in tolerance can be measured by measuring mRNA levels, or where appropriate, the level or activity of the respective protein (e.g. by means of ELISA, activity of the enzyme as measured by any technique known in the art). Endogenous gene expression refers to the expression of a protein which is naturally found in the plant, plant part or plant cell concerned.

Alternatively, said enhanced tolerance or resistance to environmental stress conditions may be achieved by introducing into the genome of the plant, one or more transgenes which interact with the expression of endogenous genes (polynucleic acids) according to the present invention, by anti-sense RNA, co-suppression or ribozyme suppression of genes which normally inhibit the expression of the polynucleic acids of the present invention or by suppression of genes which normally inhibit the activity of the polypeptides of the invention as defined above.

For inhibition of expression, the nucleic acid segment to be introduced generally will be substantially identical to at least a portion of the endogenous gene or genes to be repressed. The sequence, however, need not be perfectly identical to inhibit expression. The vectors of the present invention can be designed such that the inhibitory effect applies to other genes within a family of genes exhibiting homology or substantial homology to the target gene.

For antisense suppression, the introduced sequence also need not be full length relative to either the primary transcription product or fully processed mRNA.

Generally, higher homology can be used to compensate for the use of a shorter sequence.

5 Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments may be equally effective. Normally, a sequence of between about 30 or 40 nucleotides up to the full length sequence should be used, though a sequence of at least about 100 nucleotides is preferred, a sequence of at least about 200 nucleotides is more preferred, and a sequence of  
10 about 500 to about 1700 nucleotides is especially preferred.

Catalytic RNA molecules or ribozymes can also be used to inhibit expression of genes as explained above. It is possible to design ribozymes that specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In carrying out this cleavage,  
15 the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs.

A number of classes of ribozymes have been identified. One class of  
20 ribozymes is derived from a number of small circular RNAs which are capable of selfcleavage and replication in plants. The RNAs replicate either alone (viroid RNAs) or with a helper virus (satellite RNAs). Examples include RNAs from avocado sunblotch viroid and the satellite RNAs from tobacco ringspot virus, lucerne transient streak virus, velvet tobacco mottle virus, solanum nodiflorum mottle virus and  
25 subterranean clover mottle virus. The design and use of target RNA-specific ribozymes is described in Haseloff et al. (1988).

Another method of suppression of gene expression is sense suppression. Introduction of nucleic acid configured in the sense orientation has been shown to be an effective means by which to block the transcription of target genes. For an example  
30 of the use of this method to modulate expression of endogenous genes see, Napoli et al. (1990), and U.S. Patents Nos. 5,034,323, 5,231,020, and 5,283,184.

The suppressive effect may occur where the introduced sequence contains no coding sequence per se, but only intron or untranslated sequences homologous to sequences present in the primary transcript of the endogenous sequence. The  
35 introduced sequence generally will be substantially identical to the endogenous

sequence intended to be repressed. This minimal identity will typically be greater than about 65%, but a higher identity might exert a more effective repression of expression of the endogenous sequences. Substantially greater identity of more than about 80% is preferred, though about 95% to absolute identity would be most preferred. As with  
5 antisense regulation, the effect should apply to any other proteins within a similar family of genes exhibiting homology or substantial homology.

For sense suppression, the introduced sequence, needing less than absolute identity, also need not be full length, relative to either the primary transcription product or fully processed mRNA. This may be preferred to avoid concurrent production of  
10 some plants which are overexpressers. A higher identity in a shorter than full length sequence compensates for a longer, less identical sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and identity of non-coding segments will be equally effective. Normally, a sequence of the size ranges noted above for antisense regulation is used.

15 Other methods for altering or replacing genes known in the art can also be used to inhibit expression of a gene. For instance, insertional mutants using T-DNA or transposons can be generated. See, e.g., Haring et al. (1991) and Walbot (1992). Another strategy in genetic engineering of plants and animals is targeted gene replacement. Homologous recombination has typically been used for this purpose  
20 (see, Capecchi (1989)).

Alternatively, the present invention also relates to a method as defined above wherein said DNA encodes a sense or antisense RNA or a ribozyme capable of indirectly increasing or inducing the expression of an endogenous polynucleic acid sequence according to the invention as defined above or increasing or inducing the  
25 activity of a protein of the invention as defined above. Preferably said endogenous polynucleic acid encodes a protein as listed in Table 1.

The present invention also relates to a recombinant polynucleic acid comprising: a polynucleic acid as defined above, and, a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control  
30 of said plant-expressible promoter.

The present invention also relates to a recombinant polynucleic acid comprising:

(a) a DNA encoding a protein which when expressed in said plant at an effective amount indirectly increases or induces the expression of an endogenous

polynucleic acid as defined above or indirectly increases or induces the protein activity of a polypeptide as defined above, and,

(b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

5 An "endogenous" polynucleic acid refers to a polynucleic acid that is already present in the plant species before transformation.

Said recombinant polynucleic acid as described here above is generally also referred to as a "recombinant vector" or an "expression cassette". An expression cassette of the invention can be cloned into an expression vector by standard  
10 methods. The expression vector can then be introduced into host cells by currently available DNA transfer methods.

The present invention also relates to the recombinant polynucleic acid as defined above, comprising a DNA which encodes an anti-sense RNA, a ribozyme or a sense RNA which increases or induces the activity of a protein as defined above in  
15 said cell. Preferably said protein is listed in Table 1.

More particularly, the present invention relates to a recombinant polynucleic acid comprising at least part of the nucleotide sequence of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99,  
20 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121.

Preferably, the present invention relates to a recombinant polynucleic acid comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1. Preferably, said "part" is a unique part of any of said nucleotide sequences. (26-28) As used herein, the term a "plant-expressible promoter" refers to a promoter  
25 that is capable of driving transcription in a plant cell. This includes any promoter of plant origin, including the natural promoter of the transcribed DNA sequence, but also any promoter of non-plant origin which is capable of directing transcription in a plant cell. The promoter may also be an artificial or synthetic promoter. The term "plant-expressible promoter" includes, but is not restricted to, constitutive, inducible, organ-,  
30 tissue-specific or developmentally regulated promoters.

According to the invention, production and/or activity of a polypeptide according to the present invention in a plant or in plant parts is increased by introducing *one or more* polynucleic acids according to the invention into the genome of the plant. More specifically, the constitutive promoter can be, but is not restricted to, one of the  
35 following: a 35S promoter (Odell et al. (1985)), a 35S'3 promoter (Hull and Howell

(1987)), the promoter of the nopaline synthase gene ("PNOS") of the Ti-plasmid (Herrera -Estrella, (1983)) or the promoter of the octopine synthase gene ("POCS", De Greve et al. (1982)). It is clear that other constitutive promoters can be used to obtain similar effects. A list of plant-expressible promoters that can be used according to the present invention is given in Table 2.

For specific embodiments of this invention, the use of inducible promoters can provide certain advantages. Modulation of protein levels or protein activity may be required in certain parts of the plant, making it possible to limit modulation to a certain period of culture or developmental stage of the plant.

For specific embodiments of this invention, the use of organ- or tissue-specific or chemical inducible promoters can provide certain advantages. Thus, in specific embodiments of the invention, the gene(s) or part thereof is (are) placed under the control of a promoter directing expression in specific plant tissues or organs, such as for instance roots, leaves, harvestable parts, etc.

It is also possible to use a promoter that can be induced upon the environmental stress conditions. Such promoters can be taken for example from stress-related genes which are regulated directly by an environmental, i.e. preferable abiotic, stress in a plant cell, including genes for which expression is increased, reduced or otherwise altered. These stress related genes comprise genes the expression of which is either induced or repressed by anaerobic stress, flooding stress, cold stress, dehydration stress, drought stress, heat stress or salinity. An exemplary list of such promoters is given in Table 3.

The recombinant polynucleic acids according to the present invention may include further regulatory or other sequences from other genes, such as leader sequences (e.g. the cab22 leader from Petunia), 3' transcription termination and polyadenylation signals (e.g. from the octopine synthase gene or the nopaline synthase gene), plant translation initiation consensus sequences, introns, transcription enhancers and other regulatory elements such as adh intron 1, etc, which is or are operably linked to the gene or a fragment thereof. Additionally, the recombinant polynucleic acid can be constructed and employed to target the gene product of the polynucleic acid of the invention to a specific intracellular compartment within a plant cell on to direct a protein to the extracellular environment. This can generally be obtained by operably joining a DNA sequence encoding a transit or signal peptide to the recombinant polynucleic acid.

The recombinant DNA comprising one or more polynucleic acids according to the present invention may be accompanied by a chimeric marker gene (Hansen et al., 1999 and references therein). The chimeric marker gene can comprise a marker DNA that is operably linked at its 5' end to a plant-expressible promoter, preferably a constitutive promoter, such as the CaMV 35S promoter, or a light inducible promoter such as the promoter of the gene encoding the small subunit of Rubisco; and operably linked at its 3' end to suitable plant transcription 3' end formation and polyadenylation signals. It is expected that the choice of the marker DNA is not critical, and any suitable marker DNA can be used. For example, a marker DNA can encode a protein that provides a distinguishable color to the transformed plant cell, such as the A1 gene (Meyer et al., (1987)), can provide herbicide resistance to the transformed plant cell, such as the *bar* gene, encoding resistance to phosphinothricin (EP 0 242 246), or can provide antibiotic resistance to the transformed cells, such as the *aac(6')* gene, encoding resistance to gentamycin (WO94/01560).

According to another embodiment, the present invention relates to the use of the polynucleic acids above as selectable marker gene. More preferably, the present invention also relates to the use of the plant DBF2 gene as defined above as selectable marker gene, selection taking place with treatment with a stress condition.

The recombinant DNA vectors according to the present invention comprising the sequences from genes of the invention will typically also comprise a marker gene which confers a selectable phenotype on plant cells. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or Basta.

The present invention also relates to a recombinant host cell transformed with an isolated polynucleic acid as defined above. Said host can be any host known in the art. Preferably said recombinant host cell is a plant cell, yeast, fungi, insect cell, etc. In order to be efficiently expressed in said host, said polynucleic acids can be combined with any promoter known to function in said host system. Methods for transforming said host cells are also well known in the art.

The present invention particularly also relates to a plant cell transformed with at least one recombinant polynucleic acid as defined above.

The present invention also relates to a plant consisting essentially of plant cells transformed with at least one recombinant polynucleic acid as defined above.

A "transgenic plant" refers to a plant comprising a transgene in the genome of essentially all of its cells.

DNA constructs of the invention may be introduced into the genome of the desired plant host by a variety of conventional techniques (see for example Hansen et al., 1999 for review and WO 99/05902). For example, DNA constructs of the invention may be introduced into the genome of the desired plant host by using techniques such as protoplast transformation, biolistics or microprojectile bombardment or Agrobacterium mediated transformation.

Microinjection techniques are known in the art and well described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al. (1984).

Electroporation techniques are described in Fromm et al. (1985). Biolistic transformation techniques are described in Klein et al. (1987).

Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional Agrobacterium host vector. The virulence functions of the Agrobacterium host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. Agrobacterium tumefaciens-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example Horsch et al. (1984), and Fraley et al. (1983).

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium. Plant regeneration from cultured protoplasts is described in Evans et al. (1983); and Binding (1985). Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al. (1987).

The polynucleic acids and polypeptides of the invention can be used to confer desired traits on a broad range of plants, including monocotyledonous or dicotyledonous plants, preferably they belong to a plant species of interest in agriculture, wood culture or horticulture, such as a crop plant, root plant, oil producing plant, wood producing plant, fruit producing plant, fodder or forage legume, companion or ornamental or horticultured plant. The plants can include species from the genera Actinidia, Apium, Allium, Ananas, Arachis, Arisaema, Asparagus, Atropa, Avena, Beta,

Brassica, Carica, Cichorium, Citrus, Citrullus, Capsicum, Cucumis, Cucurbita, Cydonia, Daucus, Diospyros, Fragaria, Glycine, Gossypium, Helianthus, Heterocallis, Hordeum, Hyoscyamus, Ipomoea, Lactuca, Linum, Lolium, Lycopersicon, Malus, Mangifera, Manihot, Majorana, Medicago, Musa, Nicotiana, Oryza, Panicum, Pannesetum, Persea, Petroselinum, Phaseolus, Pisum, Pyrus, Prunus, Raphanus, Rheum, Ribes, Rubus, Saccharum, Secale, Senecio, Sinapis, Solanum, Sorghum, Spinacia, Trigonella, Triticum, Vaccinium, Vitis, Vigna, Zea, and Zingiber. Additional species are not excluded. Crops grown on cultivated lands in arid and semi-arid areas in which irrigation with ground water is needed may advantageously benefit from the invention.

One of skill will recognize that after the recombinant polynucleic acid is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. As described before, the plant cells, plant tissue, in particular, transgenic plants of the invention display a certain higher or enhanced degree of tolerance (or even resistance) to environmental stress conditions compared to the corresponding wild-type plants. For the meaning of "environmental stress", see supra. In a preferred embodiment of the present invention, the transgenic plant displays increased tolerance to osmotic stress, salt stress, cold and/or heat stress. An increase in tolerance to such environmental stress is understood to refer to a tolerance to a level of such stress which inhibits the growth and productivity of the corresponding untransformed plant, as determined by methodologies known to the art. Such increased tolerance in transgenic plants is related to an increased expression level in the transgenic plant or parts thereof of one or more of the polynucleic acids of the present invention and/or to an increased level of activity of the polypeptide(s) encoded by said polynucleic acid, as determined by methodologies known to the art. In comparison with their untransformed counterparts, and determined according to methodologies known in the art, a transgenic plant according to the present invention shows an increased growth, viability, metabolism, fertility and/or productivity under mild environmental stress conditions. In the alternative, a transgenic plant according to the invention can grow under environmental stress conditions wherein the untransformed counterparts can not grow. An increase in tolerance to salt stress is understood to refer to the capability of the transgenic plant to grow under stress conditions which inhibit the growth of at least 95% of the parent, non-stress tolerant plants from which the stress tolerant transgenic

plants are derived. Typically, the growth rate of stress tolerant plants of the invention will be inhibited by less than 50%, preferably less than 30%, and most preferably will have a growth rate which is not significantly inhibited by growth conditions which inhibit the growth of at least 95% of the parental, non-stress tolerant plants. In an alternative  
5 example, under mild environmental stress conditions, the growth and/or productivity of the transgenic plants is statistically at least 1 % higher than for their untransformed counterparts, preferably more than 5 % higher and most preferably more than 10 % higher.

Any transformed plant obtained according to the invention can be used in a  
10 conventional breeding scheme or in *in vitro* plant propagation to produce more transformed plants with the same characteristics and/or can be used to introduce the same characteristic in other varieties of the same or related species.

Furthermore, the characteristic of the transgenic plants of the present invention to maintain normal/rapid/high growth rates under environmental stress conditions can  
15 be combined with various approaches to confer environmental stress tolerance with the use of other stress tolerance genes. Some examples of such stress tolerant genes are provided in Holmberg and Bülow (1998). Most prior art approaches which include the introduction of various stress tolerance genes have the drawback that they result in reduced or abnormal growth (compared to non-transgenic controls) under normal,  
20 non-stressed conditions, namely stress tolerance comes at the expense of growth and productivity (Kasuga et al., 1999). This correlation between constitutive expression of stress-responsive genes and reduced growth rates under normal growth conditions indicates the presence of cross talk mechanisms between stress response control and growth control.

Furthermore, the characteristic of the transgenic plants of the present invention to display tolerance to environmental stress conditions can be combined with various  
25 approaches to confer to plants other stress tolerance genes, e.g., osmotic protectants such as mannitol, proline; glycine-betaine, water-channeling proteins, etc. Thus, the approach of the present invention to confer tolerance to environmental stress  
30 conditions to plants can be combined with prior art approaches which include introduction of various stress tolerance genes. Combination of these approaches may have additive and/or synergistic effects in enhancing tolerance or resistance to environmental stress.

Thus, it is immediately evident to the person skilled in the art that the method of  
35 the present invention can be employed to produce transgenic stress tolerant plant with

any further desired trait (see for review TIPTEC Plant Product & Crop Biotechnology 13 (1995), 312-397) comprising:

- (i) herbicide tolerance (DE-A 3701623; Stalker (1988)),
- (ii) insect resistance (Vaek (1987)),
- 5 (iii) virus resistance (Powell (1986), Pappu (1995), Lawson (1996)),
- (iv) ozone resistance (Van Camp (1994)),
- (v) improving the preserving of fruits (Oeller (1991)),
- (vi) improvement of starch composition and/or production (Stark (1992), Visser (1991)),
- 10 (vii) altering lipid composition (Voelker (1992)),
- (viii) production of (bio)polymers (Poirer (1992)),
- (ix) alteration of the flower color, e.g., by manipulating the anthocyanin and flavonoid biosynthetic pathway (Meyer (1987), WO90/12084),
- (x) resistance to bacteria, insects and fungi (Duering (1996), Strittmatter
- 15 (1995), Estruch (1997)),
- (xi) alteration of alkaloid and/or cardiac glycoside composition,
- (xii) inducing maintaining male and/or female sterility (EP-A1 0 412 006; EP-A1 0 223 399; WO93/25695);
- (xiii) higher longevity of the inflorescences/flowers, and
- 20 (xvi) stress resistance.

Thus, the present invention relates to any plant cell, plant tissue, or plant which due to genetic engineering displays an enhanced tolerance or resistance to environmental stress obtainable in accordance with the method of the present invention and comprising a further nucleic acid molecule conferring a novel phenotype

25 to the plant such as one of those described above.

The present invention also relates to a callus or calli consisting essentially of plant cells as defined here above. Such transgenic calli can be preferably used for the production of secondary metabolites in plant cell suspension cultures.

The present invention also relates to any other harvestable part, organ or

30 tissue or propagation material of the plant as defined here above.

The present invention also relates to the seed of a transgenic plant as defined here above, comprising said recombinant DNA.

The present invention also relates to the use of any isolated polynucleic acid as defined above to produce transgenic plants.

The present invention also relates to the use of a recombinant polynucleic acid as defined above, to produce transgenic plants, preferably transgenic plants having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

5       The present invention also relates to the use of an isolated polynucleic acid as defined above, to produce transgenic callus having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

10       The present invention also relates to probes and primers derived from the genes of the invention that are useful for instance for the isolation of additional genes having sequences which are similar to but differ from any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, but which encode a protein  
15       having substantially the same biological activity as a protein having the amino acids sequence of any of SEQ ID NO 2 to 120 (even numbers) by techniques known in the art, such as PCR. The presence of a homologous gene in another plant species can for instance be verified by means of Northern or Southern blotting experiments.

20       The present invention also relates to the cloning of the genomic counterpart of any of the cDNA sequences as represented in SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121. These genomic counterparts can be selected from a genomic library using these cDNA sequences as a probe. The present  
25       invention also relates to the coding region as well as the promoter region of any of said genomic clones.

The term "probe" according to the present invention refers to a single-stranded oligonucleotide *sequence* which is designed to specifically hybridize to any of the polynucleic acids of the invention.

30       The term "primer" refers to a single stranded oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. Preferably the primer is about 5-50 nucleotides long. The term "target region" of a probe or a primer according to the present invention is a sequence within the polynucleic acid(s) to which the probe or the  
35       primer is completely complementary or partially complementary (i.e. with some degree

of mismatch). It is to be understood that the complement of said target sequence is also a suitable target sequence in some cases.

"Specific hybridization" of a probe to a target region of the polynucleic acid(s) means that the probe forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions this probe does substantially not form a duplex with other regions of the polynucleic acids present in the sample to be analysed.

"Specific hybridization" of a primer to a target region of the polynucleic acid(s) means that, during the amplification step, said primer forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions the primer does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It is to be understood that "duplex" as used hereby, means a duplex that will lead to specific amplification.

Preferably, the probes of the invention are about 5 nucleotides to about 1 Kb long, more preferably from about 10 to 25 nucleotides. The nucleotides as used in the present invention may be ribonucleotides, deoxyribonucleotides and modified nucleotides such as inosine or nucleotides containing modified groups which do not essentially alter their hybridization characteristics. The probes according to the present invention preferably include parts of the cDNA sequences of any of the polynucleic acids as defined above.

The present invention also relates to a composition comprising a polynucleic acid sequence as defined above, a polypeptide as defined above, a probe as defined above or a primer as defined above.

The present invention also relates to a pharmaceutical or agrochemical composition comprising said polynucleic acid, a polypeptide of the invention as defined above.

The present invention also relates to antibodies specifically reacting with a protein or polypeptide according to the present invention.

The following Examples describe by way of example the tolerance and/or resistance to several environmental stress conditions observed for transgenic plants and yeast overexpressing some of the polynucleic acids according to the present invention. Unless stated otherwise in the Examples, all recombinant DNA techniques are carried out according to standard protocols as described in Sambrook et al. (1989) and in volumes 1 and 2 of Ausubel et al. (1994). Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfax (1993) by R.D.D.

Croy, jointly published by BIOS Scientific Publications Ltd. (UK) and Blackwell Scientific Publications, UK.

These examples and figures are not to be construed as limiting to any of the embodiments of the present invention as set out above. All of the references  
5 mentioned herein are incorporated by reference.

## BRIEF DESCRIPTION OF THE FIGURES AND TABLES

Figure 1. *At-DBF2* encodes a functional homolog of the yeast *Dbf2* (A) Comparison of the deduced amino acid sequence of *At-DBF2* with that of yeast *DBF2*. Gaps were introduced to optimize the alignment. Roman numerals above the *At-DBF2* sequence indicate the protein kinase catalytic subdomains defined by Hanks et al. (1988). (B) Complementation of *dbf2*. The *dbf2* mutant S7-4A [*MATa dbf2Δ::URA3 ura3 leu2 ade5 trp1 his7*] (Toyn and Johnston, 1994) (B1) forms swollen pairs of daughter cells (dumbbells) at restrictive temperature (37° C). The defective morphology of the *dbf2* mutant can be complemented by transformation with the pYX112 centromeric plasmid (Ingenius, R&D system) containing the *At-DBF2* cDNA (B2) or *DBF2* (B3); wild type (CG378 strain, *MATa ade5 leu2 trp1 ura3*) (B4). Log phase cultures were shifted from 28°C to 37°C and photographed after 16 hours. After 16 hours, 98% of the S7-4A cells arrested with a dumbbell morphology (B1) whereas 6,1 and 0% of dumbbells were observed in B1, B3 and B4. Strains were kindly provided by (Dr Lindl, Max Planck Institut für Züchtungsforschung, Köln, Germany).

Figure 2. Overexpression of *DBF2* or *At-DBF2* enhances tolerance to osmotic, salt, heat and cold stress. Yeast cells were grown in YPD and cell density was adjusted to OD600 at 2. (1) DY, (2) DY transformed with pYX212 containing *DBF2*, pYX-YDBF2, (3) DY transformed with vector alone or (4) with vector containing *At-DBF2*, pYX-AtDBF2. Serial dilutions were made in step1:10. Ten µl of each dilution was spotted on solid YPD medium (control) supplemented with 2M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) or 4µl H<sub>2</sub>O<sub>2</sub> (oxidative stress) and incubated at 28°C or at 42°C (heat stress) or at 4°C (cold stress) for 3 days.

Figure 3. *DBF2* and *At-DBF2* are induced by stress. (a) Northern analysis showing the kinetics of *At-DBF2* induction in plants treated with PEG 6000 20 % and the one of *DBF2* in yeast treated with sorbitol 2M for the time indicated. (b) Northern analysis of *At-DBF2* in 10 day-old-plants grown for 5 hours in control conditions (as described in Verbruggen et al. 1993) (1), at 37°C (2), with PEG 6000 20 % (3), NaCl 1% (4), at 4°C (5) or with 0.4 mM H<sub>2</sub>O<sub>2</sub> (6); and of *DBF2* in yeast cells grown for 11/2 hour in YPD (1), at 37°C (2), with sorbitol 2M (3), with NaCl 1.2 M (4), at 4°C (5) or with 0.4 mM H<sub>2</sub>O<sub>2</sub> (6). Control of loading has been done with EtBr staining and is shown under each Northern analysis.

(c) Western analysis of At-DBF2 in Arabidopsis. Samples are similar to those analysed in (b). Antibodies used were raised against yeast Dbf2 and kindly provided by Dr L. Leindl (Max Planck Institut für Züchtungsforschung, Köln, Germany).

5           Figure 4. *DBF2* overexpression can suppress *hog1* osmosensitivity. The *hog1* mutant (4) [W303-1A, *MATa*, *hog1Δ::TRP1*] and wild type (W303) (1) were kindly provided by Dr Thevelein (Katholieke Universiteit Leuven, Belgium). The *hog1* mutant was transformed with pYX-YDBF2 (2) or pYX-AtDBF2 (3). Each of the 4 strains was grown for 16 hours in YPD (rich medium), and cell density was adjusted to  
10   OD600 at 2. Serial dilutions, 1:10 were made at five consecutive steps. Ten microliter of each dilution was spotted on solid YPD medium (control) or solid YPD medium supplemented with 0,9 M NaCl and incubated at 28°C for 3 days.

          Figure 5. *T-DBF2* (*Nicotiana tabacum* DBF2) is periodically expressed during  
15   plant cell cycle. Tobacco *DBF2* expression has been followed in BY2 cells synchronised with aphidicolin (a & b) or with propyzamide (c & d) with *At-DBF2* as probe. The measure of relative rate of DNA synthesis and of the mitotic index, the use of the cell cycle markers *CYCB1.2* and *H4* markers have been previously described (Reicheld et al., 1995). *T-DBF2* transcript levels were quantified from the blots shown  
20   in b and d using a PhosphorImager (Molecular Dynamics).

          Figure 6. shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left  
25   section) upon applying a salt stress of 200 mM NaCl overnight.

          Figure 7 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left  
30   section) upon applying an osmotic stress induced by 20% PEG overnight.

          Figure 8 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left

section) upon applying a cold stress by gradually decreasing the temperature until – 7°C.

Figure 9 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section) upon applying a heat stress of 2 hours at 48°C.

Figure 10 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section). It can be concluded that the P35S-At-DBF2 transformed plants do not show morphological abnormalities compared to the control transgenic plants.

Figure 11 shows the results of a salt stress tolerance test with transgenic *A. thaliana* plants overexpressing HSP 17.6A (A) or c74 (B). The control plants (bottom left in A and B) is a transgenic line transformed with pBIN-35S-CaMVter. The other sections in A are 5 independently obtained transgenic lines overexpressing HSP17.6A. The other sections in B are 5 independently obtained transgenic lines overexpressing c74.

Figure 12 shows the influence of *At-DBF2* expression in sense and antisense orientations on stress tolerance. BY2 cells were transformed by *A. tumefaciens* with recombinant T-DNA vectors containing *At-DBF2* driven by CaMV 35S RNA promoter, pBIN-35S-*At-DBF2* (upper left and right sections in A or diamonds in B), the CaMV 35S promoter and terminator pBIN-35S-CaMVter (bottom left sections in A or triangles in B), or antisense *At-DBF2* under the control of the CaMV 35S promoter pBIN-35S-AS*At-DBF2* (bottom right sections in A or circles in B). (A) Picture of the same amounts of transgenic cells after 3 weeks of growth on solid medium supplemented with 300 mM NaCl, 25% PEG, 2mM H<sub>2</sub>O<sub>2</sub>, or at 47°C (heat). (B) Growth of suspension cells in liquid medium. Upon stress, growth was measured as fresh weight and expressed as a percentage of unstressed growth (control) (a). Stresses were applied after subculturing (= day 0) at indicated temperatures (e) and concentrations of NaCl (b) PEG (c), and H<sub>2</sub>O<sub>2</sub> (f). For the cold shock (d), cells were maintained at 0°C for 2 days before the 2-week culture at 22°C. For each construction data of three

independent transgenic lines were pooled. To not overload the figure, SDs are not shown (maximum 15% of measured values). (C) Northern analysis of At-DBF2+TDBF2, kin1, and HSP17.6. Total RNAs were extracted from independent lines transformed with pBIN-35S-At-DBF2 (1) and (2), pBIN-35S-CaMter (3), and pBIN-35S-  
 5 ASAt-DBF2 (4). Osmotic stress was induced with 10% PEG treatment for 5 hr (stressed).

Figure 13 shows the results of the growth of *A. thaliana* plants transformed with p35S-AtHSP17.6A and P35S control (upper right section) upon applying an osmotic  
 10 stress induced by 20% PEG overnight. The results of two independent experiments are shown, each performed with 3 independently obtained transgenic lines overexpressing At-HSP17.6A (upper left and bottom left and right).

Figure 14 shows the results of the germination of *A. thaliana* plants  
 15 transformed with p35S-Atc74 and P35S control (bottom section) on mineral medium supplemented with 125 mM NaCl. The results of two independent experiments are shown, each performed with 2 independently obtained transgenic lines overexpressing Atc74 (2 upper sections).

20

Table 1. Classification of the *Arabidopsis thaliana* clones isolated in Example 2. Clones isolated according to the description in example 2 have been analyzed on their potential to confer tolerance. According to the method described in example 2, the tolerance of different yeast transformants expressing an Arabidopsis cDNA to osmotic  
 25 stress and salt stress was compared with the tolerance of DY wild type cells.

+	:	similar growth to the DY wild type cells;
++	:	growth of the transformant is visible at a 10-fold higher dilution (1:10) than control (1:1);
+++	:	growth of the transformant is visible at a 100-fold higher dilution (1:100) than control (1:1);
30	++++	growth of the transformant is visible at a 1000-fold higher dilution (1:1000) than control (1:1).

Table 2. Exemplary plant-expressible promoters for use in the performance of  
 35 the present invention.

Table 3. Exemplary stress-inducible promoters for use in the performance of the present invention.

## **EXAMPLES**

### **Example 1. Construction of the cDNA library.**

Total RNA has been isolated from green siliques from *Arabidopsis thaliana* by grinding 1 g of siliques in 4 ml extraction buffer (100 mM tris-HCl, pH 8, 10 mM EDTA, 100 mM LiCl) at 4° C, followed by phenolisation and chloroform: isoamylalcohol (24:1) extraction. To the aqueous phase, LiCl was added up to a final concentration of 2M, and the total RNA was allowed to precipitate overnight at 4°C. After centrifugation, the pellet was redissolved in 400 µl H<sub>2</sub>O and reprecipitated with ethanol. Poly(A) messenger RNA was isolated from the total RNA by binding it to an oligo-dT cellulose spun column (Pharmacia), washing the column three times with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA, 0.5 M NaCl and eluting the mRNA with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA at 65° C.

The eluate was precipitated with ethanol, and cDNA was synthesized using MMLV- reverse transcriptase (Pharmacia) and a d(T)<sub>14</sub>-XhoI primer for the first strand and *E. coli* DNA polymerase I (Pharmacia) for the second strand.

### **Example 2. Yeast transformation and selection for osmotolerance.**

The cDNA was cloned into pYX vectors (Ingenius, R&D systems; 2 µ based pYX 212 for bank 1, ARS/CEN based pYX112 for bank 2) as EcoRI - XhoI fragments, using an Eco RI/Not I adaptor.

In these constructs, the cDNA is under the control of the strong constitutive TPI promoter. The yeast strain DY (MATa, *his3*, *can1-100*, *ade2*, *leu2*, *trp1*, *ura3::3xSV40AP1-lacZ*; kindly provided by N. Jones, Imperial Cancer Research Fund, London, UK) has been transformed with these cDNA libraries, using the Lithium Acetate transformation procedure (Gietz and Schietsl, 1995). After transformation with the Arabidopsis cDNA bank, transformants have been selected for the ability to grow in the presence of 100mM LiCl in a stepwise selection (Lee et al., 1999). LiCl is commonly used for salt tolerance screening in yeast (Haro et al. 1991). Several *A. thaliana* genes, conferring osmotolerance to the yeast, have been isolated (Table 1). To further analyse the potential of the selected Arabidopsis cDNA's to confer tolerance to environmental stress in yeast, each yeast transformant expressing such selected Arabidopsis cDNA's has been exposed to osmotic stress and salt stress. Each of the transformants was therefore grown for 16 hours in YPD (rich medium), and cell density was adjusted to OD<sub>600</sub> at 2. Serial dilutions, 1:10, were made at three consecutive

steps. Ten microliters of each dilution was spotted on solid YPD medium (control) supplemented with 2 M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) and incubated at 28°C for 3 days. The results of this drop growth test (see also Lee et al., 1999) are shown in Table 1.

5

### Example 3. Characterization of *At-DBF2*.

*At-DBF2*, a 1.8 kb cDNA (SEQ ID NO 1) has been identified in this screening that encodes a predicted 60.2 kDa protein showing 81 % similarity with the yeast Dbf2 transcriptional regulator. Homology (less than 40% similarity) has also been found with the putative Dbf2 homologues in human, *C. elegans* and *Drosophila* (named Ndr for nuclear Dbf2 related, Millward *et al.* 1995). The *At-DBF2* deduced protein sequence (SEQ ID NO 2) contains the 11 domains of protein kinases (Figure 1A). Amino acids lying between the invariant residues D and N of domain VI do not match the features of serine/threonine specificity (LKPE) defined by Hanks *et al.* (1988) but the GSPDYIALE peptide in domain VIII does well indicate serine/threonine specificity and *At-DBF2* can complement the yeast *dbf2* mutant (Figure 1B).

In mature *Arabidopsis* plants, *At-DBF2* is expressed in all tested organs. The highest abundance of transcripts has been found in siliques. A Southern analysis in *Arabidopsis*, tobacco and tomato has revealed that *DBF2* seems to be conserved in plants (see Example 13 below). As *At-DBF2* has been identified in a screening for LiCl tolerance, its effect in other stress situations has been tested in yeast (Figure 2).

### Example 4. Overexpression of *Arabidopsis* and *Saccharomyces cerevisiae* *DBF2* enhances cold, heat, salt and drought tolerance in yeast.

In order to test whether the effect was specific to the plant gene, the yeast *DBF2* gene has been overexpressed in the same vector. Upon a drop growth test (Figure 2 and Lee et al., 1999). A remarkable enhancement of stress tolerance can be seen at 42°C, during osmotic stress (sorbitol), and after salt and cold treatments in yeast. There is no difference between stress tolerance afforded by the plant or the yeast gene. The enhancement of stress tolerance due to the overexpression of *At-DBF2* or *DBF2* reflects a role for these genes in stress situations. Therefore yeast and *Arabidopsis* plants have been exposed to sorbitol- and PEG-induced osmotic stress. *At-DBF2* as well as *DBF2* is induced rapidly (1 to 2 hours) and transiently upon osmotic stress (Figure 3A). The expression of *At-DBF2* and *DBF2* has been analyzed during other environmental stresses in *Arabidopsis* plants or in yeast cells after the

time corresponding to the highest induction seen in Fig. 3A (Figure 3B). In plant as in yeast, there is a clear induction after heat, salt, osmotic and to a lesser extent after cold, which perfectly correlates with stresses to which the overexpression enhances tolerance. However, many genes are induced upon stress without relevant adaptive  
5 role, amongst others because post-transcriptional mechanisms inhibit subsequent translation. Here *At-DBF2* protein amount, as detected by anti-Dbf2 antibodies, clearly increased upon stress (Figure 3C).

**Example 5. Both *At-DBF2* and *DBF2* can functionally complement the  
10 *hog1* mutation.**

To investigate a possible interaction between stress signaling pathways and *DBF2*, the salt sensitive *hog1* mutant was transformed with *At-BDF2* and *DBF2*. The *HOG1* MAP kinase pathway regulates osmotic induction of transcription in yeast (Schuller *et al.* 1994). The osmosensitivity of the mutant could be recovered by the  
15 overexpression of both *DBF2* and *At-DBF2* (Figure 4).

**Example 6. *At-DBF2* is cell cycle regulated.**

*DBF2* expression is cell cycle regulated where it plays a role in DNA synthesis initiation but also in nuclear division through its association with the CCR4  
20 complex (Komarnitsky *et al.* 1998, Johnston *et al.* 1990). This regulation was investigated in plants. A tobacco BY-2 cell line in which the highest level of culture synchronization, compared with other plant cell lines has been achieved so far (Shaul  
*et al.* 1996, Reicheld *et al.* 1995) was used. Stationary phase cells were diluted into fresh medium and treated with aphidicolin (blocking cells in the beginning of the S  
25 phase) for 24 hours, then washed. The percentage of synchronous mitosis after release from the aphidicolin block was about 65 % (Figure 5A-B). A 1.6-Kb tobacco  
*DBF2* homologue (*T-DBF2*) could be detected on Northern blot with the *At-DBF2* as a probe. *T-DBF2* steady-state transcript level clearly oscillates during the cell cycle and  
is mainly present during S, decreases during G2 until late M from where it increases  
30 until a peak in S phase. *T-DBF2* expression occurs clearly before *CYCB1.2* (a marker of G2-M phases), but parallels the one of H4 (a S phase marker) except at the S/G2 transition, where *T-DBF2* transcripts decline earlier, and at the M/G1 transition, where  
*T-DBF2* expression increases earlier. The use of the cell cycle markers *CYCB1.2* and H4 is described in Reicheld *et al.*

To follow unperturbed G1 and S phases, BY2 cell suspension was synchronized using a double blocking procedure (Nagata *et al.*, 1992). After the release from the aphidicoline block, cells are treated for 4 hours with propyzamide in the beginning of the preprophase. The percentage of synchronous mitosis after the release from the propyzamide block was higher than 75%. *T-DBF2* was periodically expressed with an undetectable expression until late M, a sharp increase in G1 and a peak in mid S (Figure 5C-D) which confirms results of Figures 5A-B. However a function for the plant *DBF2* in cell cycle can only be assigned with measurement of the kinase activity. In yeast, *DBF2* transcript levels do not correlate with kinase activation which occurs by dephosphorylation (Toyn and Johnson, 1994). The precise function of Dbf2 in regulation of the cell cycle is not known. An essential role has been proposed during anaphase or telophase. No activity has been measured in G1 despite evidence for a role for Dbf2 in initiation of DNA synthesis.

As other proteins recently identified, Dbf2 controls the M/G1 transition which is a major cell cycle transition in yeast (Aerne *et al.* 1998). The existence of a M/G1 control checkpoint has been suggested in plant cells (Hemmerlin and Bach 1998) but its importance compared to G1/S and G2/M has not been investigated.

Overexpression of *DBF2* in yeast results in kinase activity throughout the cell cycle, which may be due to the saturation of a post-translational deactivating mechanism (Toyn and Johnston, 1994). Overexpression of the functionally conserved *At-DBF2* has most probably the same effect. However, the presence of Dbf2 kinase activity at the wrong time in the cell cycle does apparently not affect its progression. In marked contrast constitutive activity has a marked effect on stress tolerance. The role played by *At-DBF2* or *DBF2* in stress is most probably independent from the cell division cycle. *At-DBF2* expression is present in all plant organs (abundant expression is observed in stems where only 1-2 % cells have a mitotic activity) and can be rapidly induced upon stress. However, a link with the cell cycle is not excluded. Higher stress tolerance in yeast overexpressing *DBF2* or *At-DBF2* may be correlated to the overproduction of the kinase in G1 where yeast cells are particularly sensitive to stress. Most plant cells are also thought to be blocked in G1 but the relationship with stress response is poorly known.

**Example 7. Tobacco cell transformation and recombinant T-DNA Vector construction**

BY2 cells were stably transformed as described (Shaul et al., 1996) by *Agrobacterium tumefaciens* C58C1Rif<sup>R</sup> (pGV2260) strain (Deblaere et al., 1985) carrying pBIN-35S-At-DBF2 or pBIN-35S-ASAt-DBF2 recombinant binary vectors. PBIN-35S-At-DBF2 is the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp reporter gene was replaced with a BamHI-SacI fragment containing the At-DBF2 cDNA from pYX-At-DBF2. p-Bin-35S-CaMVter is the plant binary vector pBIN19 in the HindIII-SacI restriction sites of which the hindIII-SacI fragment of pDH51 containing the cauliflower mosaic virus (CaMV) 35S RNA promoter and terminator was cloned. pBIN-35S-ASAt-DBF2 is the pBIN-35S-CaMVter vector in which the At-DBF2 cDNA was cloned in the antisense orientation from pYXAt-DBF2 in the BamHI-SmaI restriction sites, between the CaMV 35S RNA promoter and terminator. More details are described in Lee et al. (1999).

15

**Example 8. Overexpression of At-DBF2 sense and antisense RNA in plant cells**

Transgenic plant cells overexpressing *At-DBF2* were generated to test the role of this protein in stress tolerance *in planta*. Tobacco BY2 cells were stably transformed by *A. tumefaciens* carrying the *At-DBF2* cDNA driven by the strong constitutive CaMV 35S RNA promoter. The antisense *At-DBF2* RNA also was overexpressed under the control of the same promoter. Control lines were obtained by transforming tobacco BY2 cells with pBIN-35S-CaMVter. Three independently obtained *At-DBF2*-overexpressing tobacco transgenic cell lines have been selected with a high and similar *At-DBF2* expression and analysed further. Three tobacco transgenic cell lines overexpressing antisense *At-DBF2* were chosen that showed an undetectable tobacco DBF2 transcript level. Both the overexpression of *At-DBF2* and the down-regulation of the endogenous gene by the antisense strategy did not result in significant differences in growth after 2 weeks (Fig. 12A and 12B). On the contrary, marked differences in growth were observed after a 2-week treatment with NaCl, PEG-induced drought, cold, or high temperatures. Transgenic lines that overexpressed *At-DBF2* were clearly more tolerant than control lines. Inhibition of the endogenous DBF2 expression was correlated with a higher sensitivity to those stresses. To understand the basis of stress

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tolerance in *At-DBF2*-overexpressing plant cells, expression of stress-induced genes was followed in control and stress conditions (Fig. 12C). Tobacco kin1 and HSP17.6A homologues already were induced in *At-DBF2*-overexpressing tobacco cells in control conditions to a level similar to that observed during stress conditions (PEG-induced drought), suggesting that *At-DBF2* overexpression may mimic a stress signal.

#### **Example 9. Arabidopsis transformation and recombinant T-DNA vector construction with genes conferring tolerance to environmental stress**

Arabidopsis were stably transformed as described in Clarke, Wei and Lindsey (1992) by *Agrobacterium tumefaciens* C58C1Rif<sup>R</sup> (pGV2260) strains carrying pBIN-35S-*At-DBF2*, pBIN-35S-*At-HSP17.6A*, pBIN-35S-*At-c74* recombinant binary vectors. pBIN-35S-*At-DBF2* is described in Lee et al. 1999. pBIN-35S-*At-HSP17.6A* recombinant binary vector was constructed as following: the EcoRI-XhoI fragment containing *At-HSP17.6A* cDNA in pYX-HSP17.6A (recombinant pYX212) was first cloned in pYES2 (Invitrogen) resulting in pYES-HSP17.6A. Then the BamHI-SphI fragment of pYES-HSP17.6A containing the *At-HSP17.6A* cDNA was cloned in the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp receptor gene was deleted and replaced by the *At-HSP17.6A* cDNA. The 3' protruding ends generated by SacI and SphI were blunt ended by T4 DNA polymerase. pBIN-35S-*c74* was constructed with a similar strategy as pBIN-35S-*AtHSP17.6A* with an intermediary pYES-*Atc74* vector. The *At-c74* cDNA was first amplified with PCR using the primers 5' AAA AAA CAC ATA CAG GAA TTC 3' (SEQ ID NO 122) and 5' AGT TAG CTA GCT GAG CTC GAG 3' (SEQ ID NO 123), then cloned "blunt ended" in the vector pYES2 cut with NotI and BstXI and blunt ended with T4 DNA polymerase. Subsequently, the BamHI-SphI fragment of pYES-*c74* was cloned in pBINm-gfp4 as explained supra.

#### **Example 10. Tolerance to environmental stress in plant cells**

Transgenic calli were isolated from each of the transgenic Arabidopsis lines transformed with *At-DBF2*, *At-HSP17.6A* and *At-c74*. The growth of these transgenic calli during salt stress was measured and compared with control calli derived from transgenic Arabidopsis lines transformed with pBIN-35S-*CaMVter*. Callus pieces (25 for each transgenic line) of similar fresh weight (50 to 100 mg) were therefor grown on callus inducing medium (Clarke et al., 1992) supplemented with 200mM NaCl. After two weeks, from visual inspection, it was clear that transgenic calli transformed with

At-DBF2 or At-HSP17.6A or At-c74 looked much better than control transgenic calli transformed with pBIN-35S-CaMVter. The latter calli turned yellow and started dying. To confirm the observation, the fresh weight of the calli was measured. In comparison with the control transgenic calli, the fresh weight of the transgenic calli was for each of the three lines at least five times higher than the fresh weight of the control transgenic calli.

#### **Example 11. Tolerance to environmental stress in plants.**

Seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, p-BIN-35S-At-c74, or pBIN-35S-At-HSP17.6A, were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-AS+At-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 200 mM NaCl for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2 or At-HSP17.6A or At-c74 survived very well (Figure 6 and Figure 11).

To further evaluate the scope of protection to environmental stress, transgenic plants were exposed to osmotic stress. Therefore seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, pBIN-35S-At-c74 or pBIN-35S-At-HSP17.6A were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark,

70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 20 % polyethylene glycol for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2, At-HSP17.6A or At-c74 survived very well (see Figure 7 and 13). Their growth was comparable to growth on control medium without polyethylene glycol.

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to high and low temperatures. Therefor seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, for the experiments with high temperature stress, plants were exposed to 48°C for two hours. For the experiments with low temperature stress, plants were exposed to gradually decreasing temperatures, down to -7°C. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium.

Under both low temperature and high temperature stress, the growth of control transgenic plants was inhibited and eventually they died. The transgenic lines transformed with At-DBF2 or At-c74 survived very well. Their growth was comparable to growth under control conditions with normal temperature (see Figure 8 and 9).

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to salt stress during germination. Sterilized mature seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were placed on top of petri dishes containing MS (Murashige and Skoog) medium with 0,8 % agar and 30 g l<sup>-1</sup> sucrose. Control plants were the ones transformed with pBIN-35S-CaMVter. Prior to germination and pH 5.7 adjustment, NaCl was added to a final concentration of 125 mM. Three petri dishes with a mean of 40-50 seeds per dish were used per treatment in every experiment. The complete experiment was repeated

twice. Seed germination at 22°C was followed. Seeds were considered to germinate after radical and green cotyledon emergency occurred.

On control medium (without 125 mM NaCl), germination of all transgenic lines was very similar to each other and to wild type plants. On medium supplemented with 125 mM NaCl, seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate significantly better than control transgenic lines. Less than 10 % of the seeds from transgenic lines transformed with pBIN-35S-CaMVter germinate under these conditions. In contrast, more than 70 % of the seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate on medium containing 125 mM NaCl (Figure 14).

#### Example 12. Southern hybridisation of At-DBF2 genes in other plants

To investigate whether *DBF2* homologues exist in other plant species, a Southern hybridisation analysis was performed using the full length *At-DBF2* as a probe. Genomic DNA was extracted from tobacco, tomato and rice according to Dellaporta et al. (1983) and further purified by phenol :chloroform extractions.

DNA (10 µg) was digested with restriction enzymes and separated on 1% (w/v) agarose gels using Lambda DNA digested with Hind III as molecular size standards. The DNA was transferred on to nylon membranes (Hybond N ; Amersham, little Chalfont, UK) in 0.4 N NaOH. Filters were UV-cross-linked for 30 seconds, prehybridized for 3 hours at 56°C in hybridization solution (2x SSPE, 0.1%(w/v) SDS, 5x Denhardt solution) using 200 gm<sup>-3</sup> denatured salmon sperm DNA, and hybridized overnight with radiolabelled probes. 1X SSPE was 0.15 M NaCl/ 0.01 M sodium dihydrogen phosphate/ 1 mM EDTA

Filters were washed at 56°C in 2x SSPE, 0.1% (w/v) SDS for 20 min, then 1x SSPE, 0.1% (w/v) SDS for 20 min, and finally in 0.1x SSPE, 0.1% (w/v) SDS for 20 min. Filters were exposed to X-ray film (Kodak X-AR ; Kodak, NY, USA) in the presence of intensifying screens for 24 hours.

The results of the hybridisation experiments show that tobacco, tomato and rice have at least one homologue to At-DBF2.

Tabel 1

putative function in	Features of encoded protein	SEQ ID NO.	Growth on medium with 1,2 M NaCl	growth on medium with 2,0 M sorbitol
signalling	Similar to a yeast DBF2 cell cycle protein	1	++++	++++
metabolism	HSP17.6A	3	++++	++++
unknown	C74	5	+++	+++
metabolism	Similar to ADH2	7	+	++++
metabolism	Similar to D. melanogaster catalase/catalase 3	9	++++	+
metabolism	Similar to the HSP90 heat shock protein family	11	++++	++++
metabolism	similar to phosphoenolpyruvate carboxylase	13	+	+++
metabolism	pathogen related proteins, class 10	15	+	++++
metabolism	Arabidopsis ascorbate peroxidase	17	++++	++++
metabolism	similar to phosphatase binding protein	19	++++	++++
metabolism	similar to phosphatase binding protein	21	++++	++++
metabolism	similar to retinol dehydrogenase	23	+++	++++
metabolism	similar to retinol dehydrogenase	25	++++	++++
metabolism	ribosomal protein	27	++++	++++
metabolism	ribosomal protein	29	++++	++++
metabolism	similar to a protein transporter (kinase homolog)	31	++++	++++
metabolism	similar to a peptide transporter	33	++++	+
metabolism	similar to a wheat low affinity cation transporter LCT1	35	++++	++++
metabolism	similar to yeast iso-1-cytochrome c (CYC-1)	37	++++	++++
metabolism	similar to yeast OSM1	39	++++	++++
metabolism	similar to yeast copper uptake gene (CUP1)	41	++++	+++
metabolism	similar to yeast UV-induced damage repair protein (RAD7)	43	++++	++++
metabolism	electron transporter, apocytochrome b	45	++++	++++
metabolism	similar to membrane lipoprotein LPPL1	47	++++	++++
metabolism	similar to tobacco auxin binding protein	49	+	++++
metabolism	similar to tobacco cytokinin binding protein CBP 57	51	+++	++++
signalling	similar to calcium binding protein yeast calcineurin B	53	+++	++++

signalling	similar to calcium binding protein glycine max calnexin	55	++++	+++
signalling	similar to calcium binding protein Dictyostelium discoideum calreticulin	57	++++	++++
signalling	similar to calcium binding protein calmodulin 1	59	++++	+
signalling	similar to calcium binding protein calmodulin 2	61	+	++++
signalling	MAP kinase kinase, homologous to Dictyostelium mekA (DdMek1)	63	++++	+++
signalling	similar to human adenosine kinase	65	+	++++
signalling	similar to human tyrosine kinase	67	++++	++++
signalling	similar to common ice plant tyrosine kinase	69	++++	++++
signalling	similar to the yeast protein kinase C receptor	71	++++	++++
signalling	similar to tobacco and Arabidopsis HAT7 homeotic protein	73	++	++++
signalling	similar to E. coli sigma factor regulator (RSEB)	75	+	++++
signalling	similar to human protein phosphatase 2C	77	++++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	79	++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	81	++	++++
metabolism	pathogen related proteins, class 10	83	++++	++++
metabolism	cell wall peroxidase	85	++++	+++
metabolism	ribosomal protein	87	+++	++++
metabolism	salt stress induced protein, SAS 1	89	++++	++++
metabolism	PR gene (AIG2)	91	++++	++++
metabolism	MT1c	93	++++	++++
metabolism	IPP2 (Isopentenyl diphosphate)	95	+++	++++
metabolism	chlorophyll a/b binding protein	97	+++	+++
metabolism	glutathione transferase	99	++	++++
signalling	cold- and ABA inducible, calcium dependent - kinase, Kin1	101	++++	++++
signalling	MAP kinase, Atmpk1	103	++	++++
signalling	Arabidopsis cell cycle protein histone H2A	105	++++	++++
unknown	chromosome 4 - sequence	107	+++	++++
unknown	chromosome 4 - sequence	109	+	++++
unknown	chromosome 5 - sequence	111	++++	+++
unknown	chromosome 5 - sequence	113	++++	++
unknown	chromosome 5 - sequence	115	++++	++++
unknown	chromosome 5 - sequence	117	+	++++
unknown	chromosome 5 - sequence	119	+	++++

signalling	similar to calcium binding protein centrin (caltractin)	121	++++	++++
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**TABLE 2**  
**EXEMPLARY PLANT-EXPRESSIBLE PROMOTERS FOR USE IN THE PERFORMANCE OF**  
**THE PRESENT INVENTION**

GENE SOURCE	EXPRESSION PATTERN	REFERENCE
$\alpha$ -amylase ( <i>Amy32b</i> )	Aleurone	Lanahan <i>et al.</i> (1992); Skriver <i>et al.</i> (1991)
cathepsin $\beta$ -like gene	Aleurone	Cejudo <i>et al.</i> (1992)
<i>Agrobacterium rhizogenes</i> <i>rolB</i>	Cambium	Nilsson <i>et al.</i> (1997)
PRP genes	cell wall	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
barley <i>ltr1</i> promoter	Endosperm	
synthetic promoter	Endosperm	Vicente-Carbajosa <i>et al.</i> (1998)
AtPRP4	Flowers	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
chalcone synthase ( <i>chsA</i> )	Flowers	van der Meer <i>et al.</i> (1990)
<i>apetala-3</i>	Flowers	
Chitinase	fruit (berries, grapes, etc)	Thomas <i>et al.</i> CSIRO Plant Industry, Urrbrae, South Australia, Australia; <a href="http://winetitles.com.au/gwrdc/csh95-1.html">http://winetitles.com.au/gwrdc/csh95-1.html</a>
<i>rbcS-3A</i>	green tissue (eg leaf)	Lam <i>et al.</i> (1990); Tucker <i>et al.</i> (1992)
leaf-specific genes	Leaf	Baszczynski <i>et al.</i> (1988)
AtPRP4	Leaf	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
<i>Pinus cab-6</i>	Leaf	Yamamoto <i>et al.</i> (1994)
SAM22	Senescent leaf	Crowell <i>et al.</i> (1992)
<i>R. japonicum nif</i> gene	Nodule	United States Patent No. 4, 803, 165
<i>B. japonicum nifH</i> gene	Nodule	United States Patent No. 5, 008, 194

GmENOD40	Nodule	Yang <i>et al.</i> (1993)
PEP carboxylase (PEPC)	Nodule	Pathirana <i>et al.</i> (1992)
Leghaemoglobin (Lb)	Nodule	Gordon <i>et al.</i> (1993)
<i>Tungro bacilliform</i> virus gene	Phloem	Bhattacharyya-Pakrasi <i>et al.</i> (1992)
sucrose-binding protein gene	plasma membrane	Grimes <i>et al.</i> (1992)
pollen-specific genes	pollen; microspore	Albani <i>et al.</i> (1990); Albani <i>et al.</i> (1991)
maize pollen-specific gene	Pollen	Hamilton <i>et al.</i> (1992)
sunflower pollen-expressed gene	Pollen	Baltz <i>et al.</i> (1992)
<i>B. napus</i> pollen-specific gene	pollen; anther; tapetum	Arnoldo <i>et al.</i> (1992)
root-expressible genes	Roots	Tingey <i>et al.</i> (1987); An <i>et al.</i> (1988);
tobacco auxin-inducible gene	root tip	Van der Zaal <i>et al.</i> (1991)
$\beta$ -tubulin	Root	Oppenheimer <i>et al.</i> (1988)
Tobacco root-specific genes	Root	Conkling <i>et al.</i> (1990)
<i>B. napus</i> G1-3b gene	Root	United States Patent No. 5, 401, 836
SbPRP1	Roots	Suzuki <i>et al.</i> (1993)
AtPRP1; AtPRP3	roots; root hairs	<a href="http://salus.medium.edu/mmq/tierney/html">http://salus.medium.edu/mmq/tierney/html</a>
RD2 gene	root cortex	<a href="http://www2.cnsu.edu/ncsu/research">http://www2.cnsu.edu/ncsu/research</a>
TobRB7 gene	root vasculature	<a href="http://www2.cnsu.edu/ncsu/research">http://www2.cnsu.edu/ncsu/research</a>
AtPRP4	leaves; flowers; lateral root primordia	<a href="http://salus.medium.edu/mmq/tierney/html">http://salus.medium.edu/mmq/tierney/html</a>
Seed-specific genes	Seed	Simon <i>et al.</i> (1985); Scofield <i>et al.</i> (1987); Baszczyński <i>et al.</i> (1990)
Brazil Nut albumin	seed	Pearson <i>et al.</i> (1992)
Legumin	Seed	Ellis <i>et al.</i> (1988)
Glutelin (rice)	Seed	Takaiwa <i>et al.</i> (1986); Takaiwa <i>et al.</i>

		(1987)
Zein	Seed	Matzke <i>et al.</i> (1990)
NapA	Seed	Stalberg <i>et al.</i> (1996)
Sunflower oleosin	seed(embryo and dry seed)	Cummins <i>et al.</i> (1992)
<i>LEAFY</i>	shoot meristem	Weigel <i>et al.</i> (1992)
<i>Arabidopsis thaliana knat1</i>	shoot meristem	Accession number AJ131822
<i>Malus domestica kn1</i>	shoot meristem	Accession number Z71981
<i>CLAVATA1</i>	shoot meristem	Accession number AF049870
Stigma-specific genes	Stigma	Nasrallah <i>et al.</i> (1988); Trick <i>et al.</i> (1990)
Class I patatin gene	Tuber	Liu <i>et al.</i> (1991)
<i>Blz2</i>	Endosperm	EP99106056.7
PCNA rice	Meristem	Kosugi <i>et al.</i> (1991); Kosugi and Ohashi (1997)

**Table 3. Stress inducible promoters**

<b>Name</b>	<b>Stress</b>	<b>Reference</b>
P5CS (delta(1)-pyrroline-5-carboxylate syntase)	salt, water	Zhang et al; Plant Science. Oct 28 1997; 129(1): 81-89
cor15a	Cold	Hajela et al., Plant Physiol. 93: 1246-1252 (1990)
cor15b	Cold	Wlihelm et al., Plant Mol Biol. 1993 Dec; 23(5):1073-7
cor15a (-305 to +78 nt)	cold, drought	Baker et al., Plant Mol Biol. 1994 Mar; 24(5): 701-13
rd29	salt, drought, cold	Kasuga et al., Nature Biotechnology, vol 18, 287-291, 1999
heat shock proteins, including artificial promoters containing the heat shock element (HSE)	Heat	Barros et al., Plant Mol Biol, 19(4): 665-75, 1992. Marrs et al., Dev Genet., 14(1): 27-41, 1993. Schoffl et al., Mol Gen Gent, 217(2-3): 246-53, 1989.
smHSP (small heat shock proteins)	heat	Waters et al, J Experimental Botany, vol 47, 296, 325-338, 1996
wcs120	Cold	Ouellet et al., FEBS Lett. 423, 324-328 (1998)
ci7	Cold	Kirch et al., Plant Mol Biol, 33(5): 897-909, 1997 Mar
Adh	cold, drought, hypoxia	Dolferus et al., Plant Physiol, 105(4): 1075-87, 1994 Aug
pws18	water: salt and drought	Joshee et al., Plant Cell Physiol, 39(1): 64-72, 1998, Jan
ci21A	Cold	Schneider et al., Plant Physiol, 113(2): 335-45, 1997
Trg-31	Drought	Chaudhary et al., Plant Mol Biol, 30(6): 1247-57, 1996
Osmotin	Osmotic	Raghothama et al., Plant Mol Biol, 23(6): 1117-28, 1993

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**Claims**

1. A method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.
2. An isolated polynucleic acid obtainable by a method according to claim 1.
3. The isolated polynucleic acid of claim 2 which encodes a polypeptide as listed in Table 1.
4. The isolated polynucleic acid of claim 3, which is chosen from:
  - (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or the complementary strands thereof;
  - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
  - (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
  - (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).
5. The isolated polynucleic acid of any of claim 2 to 4, which encodes a plant homolog of yeast DBF2 kinase.
6. The isolated polynucleic acid of claim 5, which is chosen from:
  - (a) SEQ ID NO 1, or the complementary strands thereof;
  - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

5

7. Use of an isolated polynucleic acid of claims 2 to 3 which encodes an HSP 17.6A protein for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

- 10 8. Use of an isolated polynucleic acid of claim 7 for expression of the protein encoded thereby in a plant cell, with said polynucleic acid being chosen from:

- (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- 15 (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of
- 20 (a) to (c).

9. Use of an isolated polynucleic acid as defined above which is chosen from:

- (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;
- 25 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 30 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

- 35 for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

10. The isolated polynucleic acid of any of claims 2 to 4, which encodes a c74 protein which is chosen from:

- (a) SEQ ID NO 5, or the complementary strand thereof;
- 5 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- 10 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

11. An isolated polypeptide encoded by a polynucleic acid according to or as defined  
15 in any of claims 2 to 10, or a functional fragment thereof.

12. The isolated polypeptide of claim 11 having at least part of the sequence of any of  
SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40,  
42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84,  
20 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or  
120.

13. A method for producing a plant with enhanced tolerance or resistance to  
environmental stress, said method comprising transiently introducing into a plant  
25 cell a recombinant DNA comprising a polynucleic acid of or as defined in any of  
claims 2 to 10 which is expressed in an amount effective to confer enhanced  
tolerance or resistance to environmental stress.

14. A method for producing a plant with enhanced tolerance or resistance to  
30 environmental stress, said method comprising stably introducing into a plant cell a  
recombinant DNA comprising a polynucleic acid of or as defined in any of claims 2  
to 10 which is expressed in an amount effective to confer enhanced tolerance or  
resistance to environmental stress.

15. The method of claims 13 or 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 5 or 6 encoding a plant DBF2 kinase.
- 5
16. The method of claim 16 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 7 or 8 encoding an HSP 17.6A protein.
- 10
17. The method of claim 13 to 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claim 10 encoding a c74 protein.
18. The method of any of claims 13 to 17, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
- 15
- a polynucleic acid according to or as defined in any of claims 2 to 10, and,
  - a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 20
19. A method for producing a plant with enhanced tolerance or resistance to environmental stress, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
- 25
- a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or indirectly increases or induces the activity of a polypeptide of claims 11 or 12, and,
- 30

- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

5 20. A method of claim 19 wherein said DNA encodes a sense or antisense RNA molecule or a ribozyme capable of increasing or inducing the expression of said endogenous polynucleic acid sequence according to or as defined in any of claims 2 to 10.

10 21. A recombinant polynucleic acid comprising:  
a polynucleic acid according to or as defined in any of claims 2 to 10, and,  
a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.

15 22. A recombinant polynucleic acid comprising:  
(a) a DNA encoding a protein which when expressed in said plant cell at an effective amount increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or increases or induces the activity of a polypeptide of claims 11 or 12, and,  
20 (b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

23. The recombinant polynucleic acid of claim 22, wherein said DNA encodes an anti-sense RNA, a ribozyme or a sense RNA which when expressed in a cell of a plant  
25 increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or which induces or increases the activity of a protein of claim 11 or 12.

24. The recombinant polynucleic acid of claim 21 comprising at least part of the  
30 nucleotide sequence of any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or part thereof.

25. The recombinant polynucleic acid of claim 21 to 24 comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1.
26. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a constitutive promoter.
27. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a stress-inducible or organ- or tissue-specific promoter.
28. The recombinant polynucleic acid of any of claims 21 to 26 wherein said plant-expressible promoter is the 35S promoter of CaMV.
29. A recombinant host cell transformed with at least one isolated polynucleic acid of or as defined in any of claims 2 to 10.
30. A plant cell transformed with a recombinant polynucleic acid of any one of claims 21 to 28.
31. A plant consisting essentially of plant cells of claim 30.
32. A callus consisting essentially of plant cells of claim 30.
33. A harvestable part, organ, tissue or propagation material of a plant of claim 31, comprising said recombinant DNA.
34. The use of a recombinant polynucleic acid of claim 21 to 28 to produce transgenic plants.
35. A probe which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which hybridizes specifically with said polynucleic acid or the complement thereof.
36. A primer which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which specifically amplifies said polynucleic acid or the complement thereof.

37. A composition comprising a polynucleic acid sequence of or as defined in any of claims 2 to 10, a polypeptide of claim 11 or 12, a probe of claim 35 or a primer of claim 36.

[illegible]

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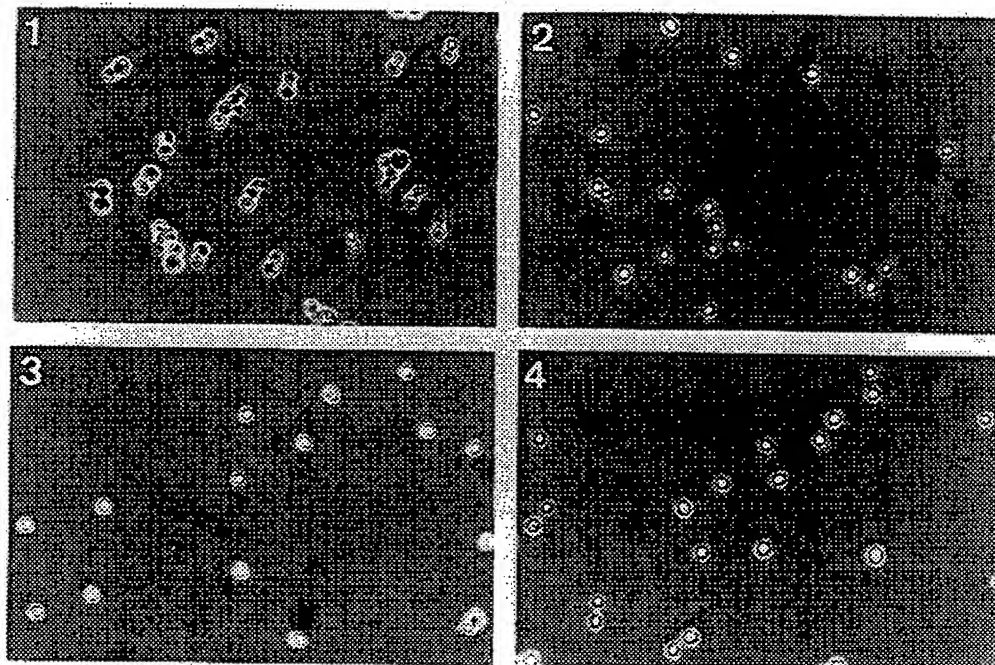


FIGURE 1B

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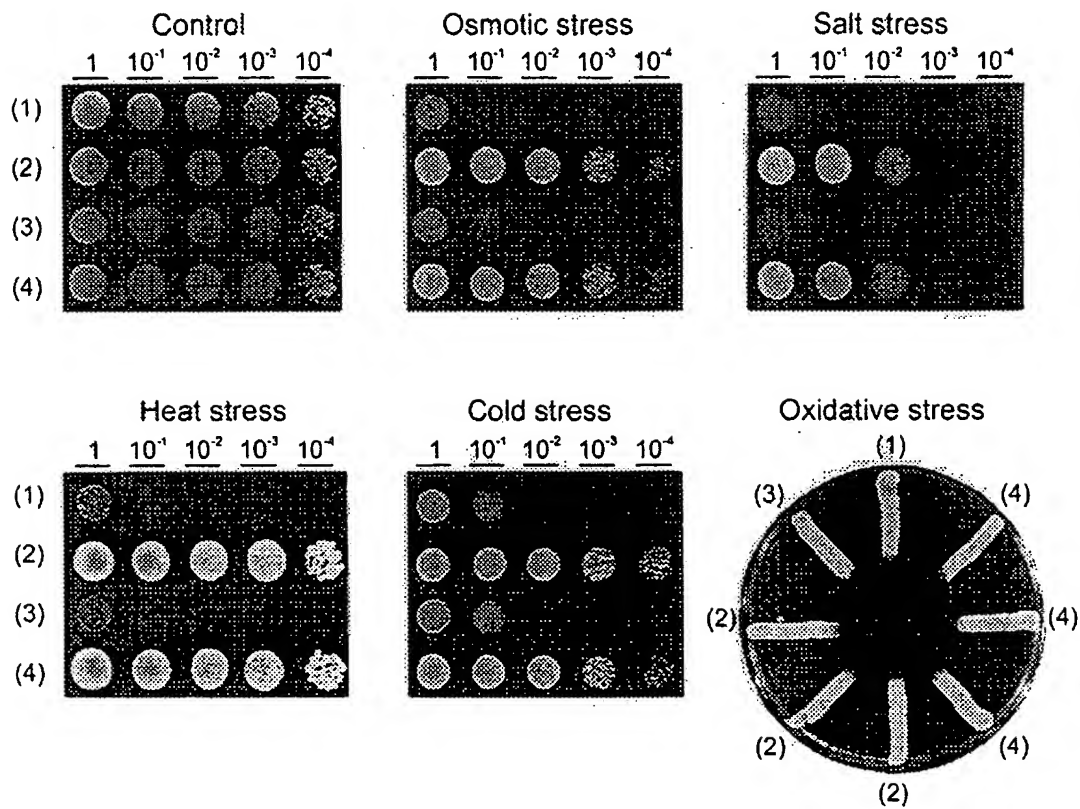


FIGURE 2

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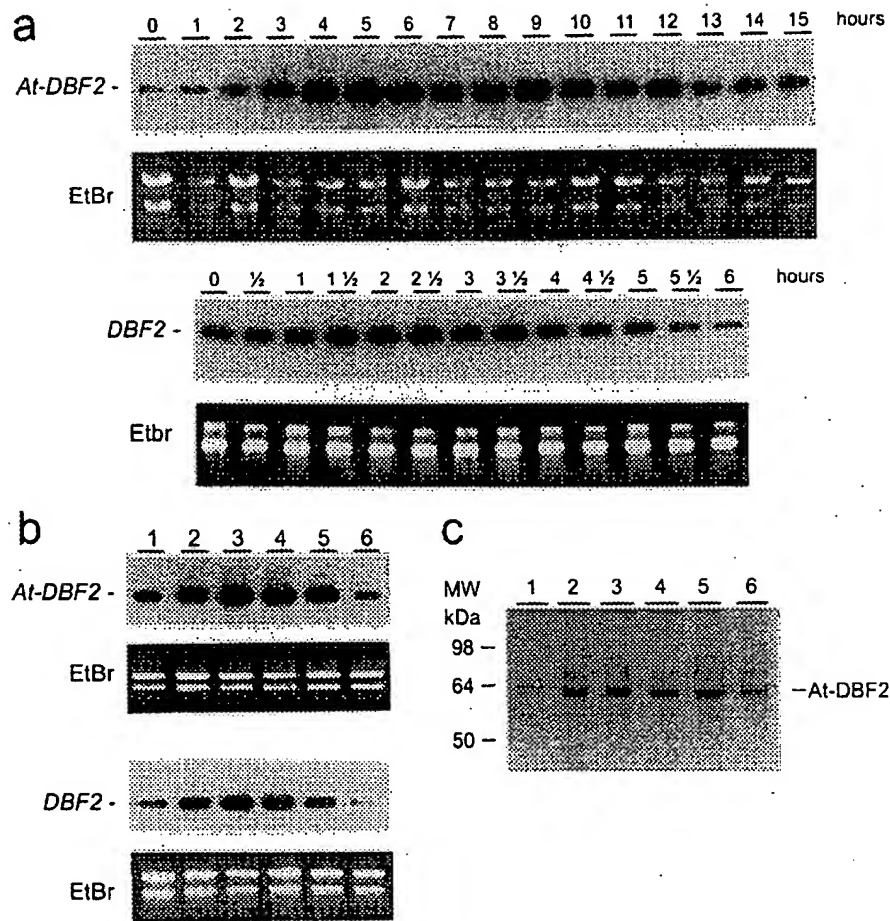


FIGURE 3

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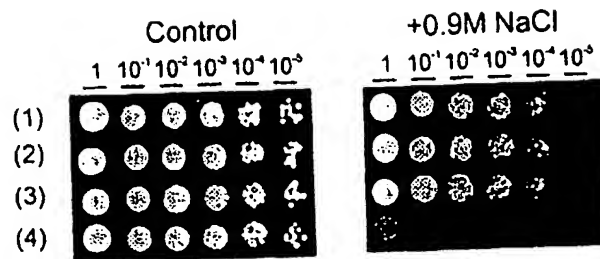


FIGURE 4

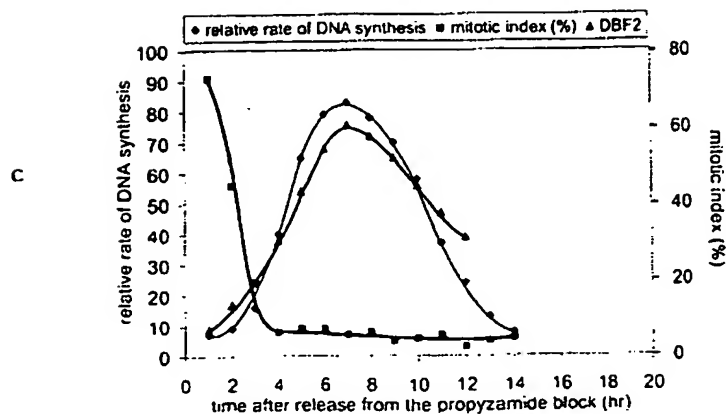
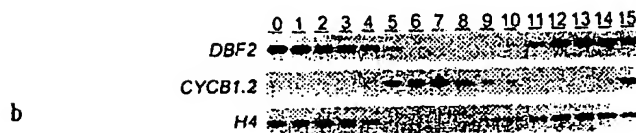
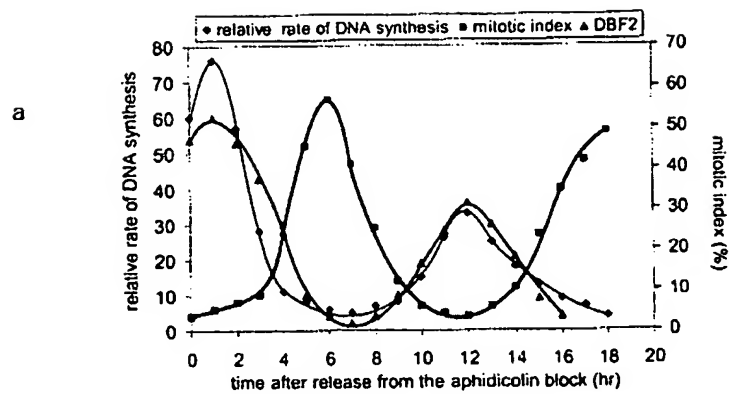


FIGURE 5

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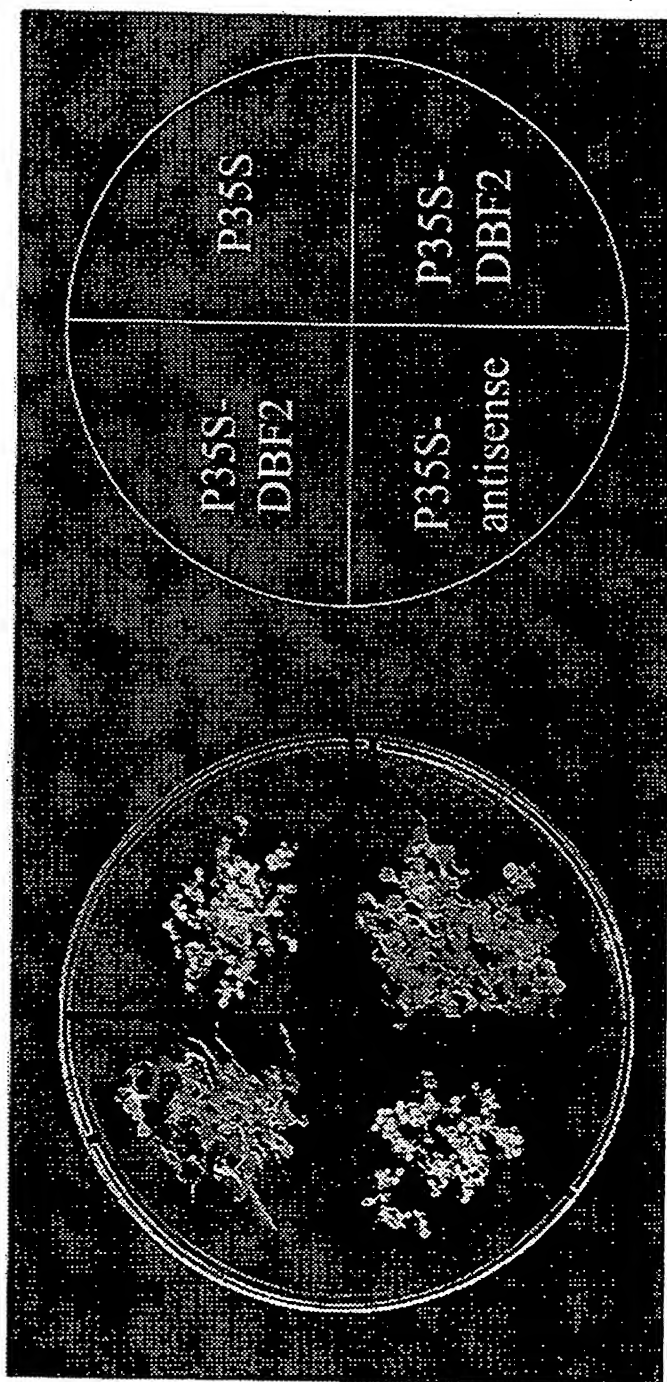


FIGURE 6

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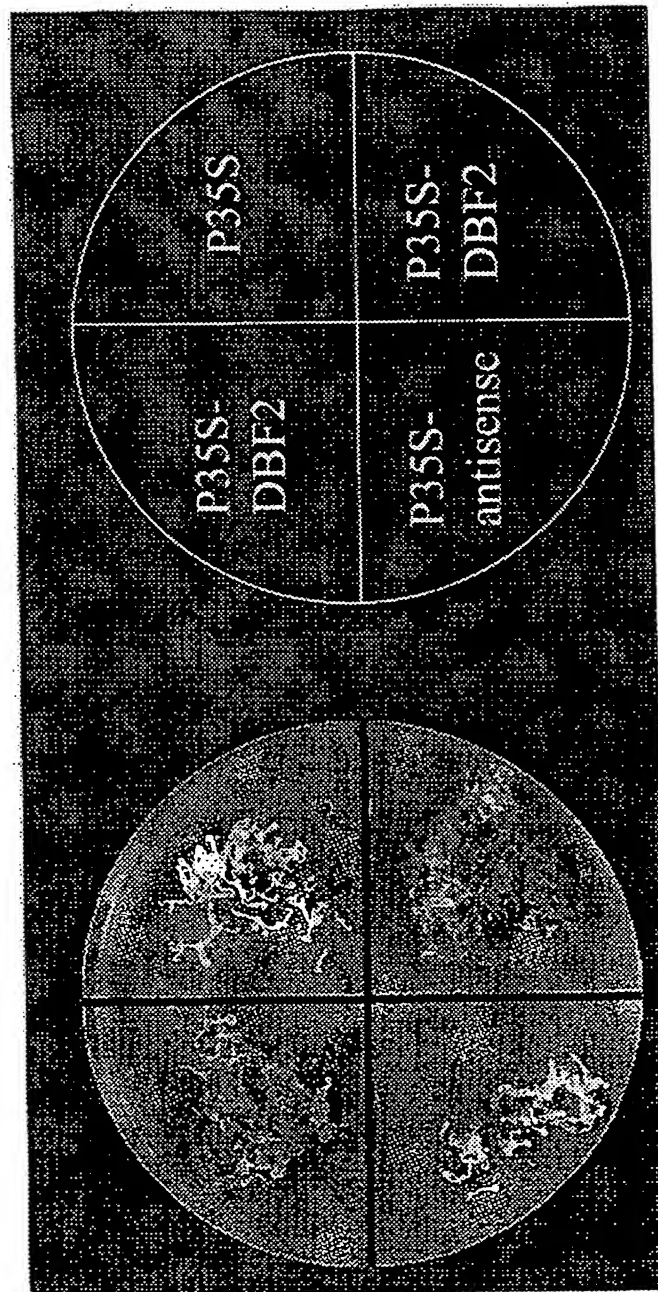


FIGURE 7

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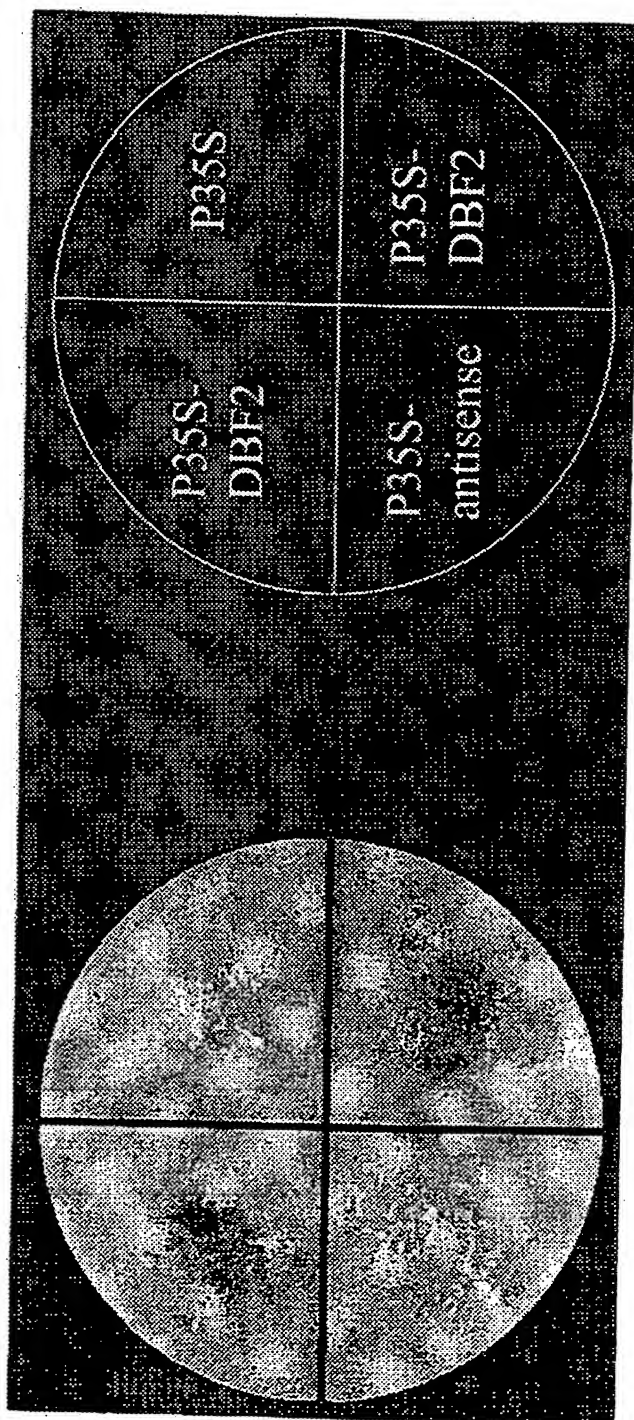


FIGURE 8

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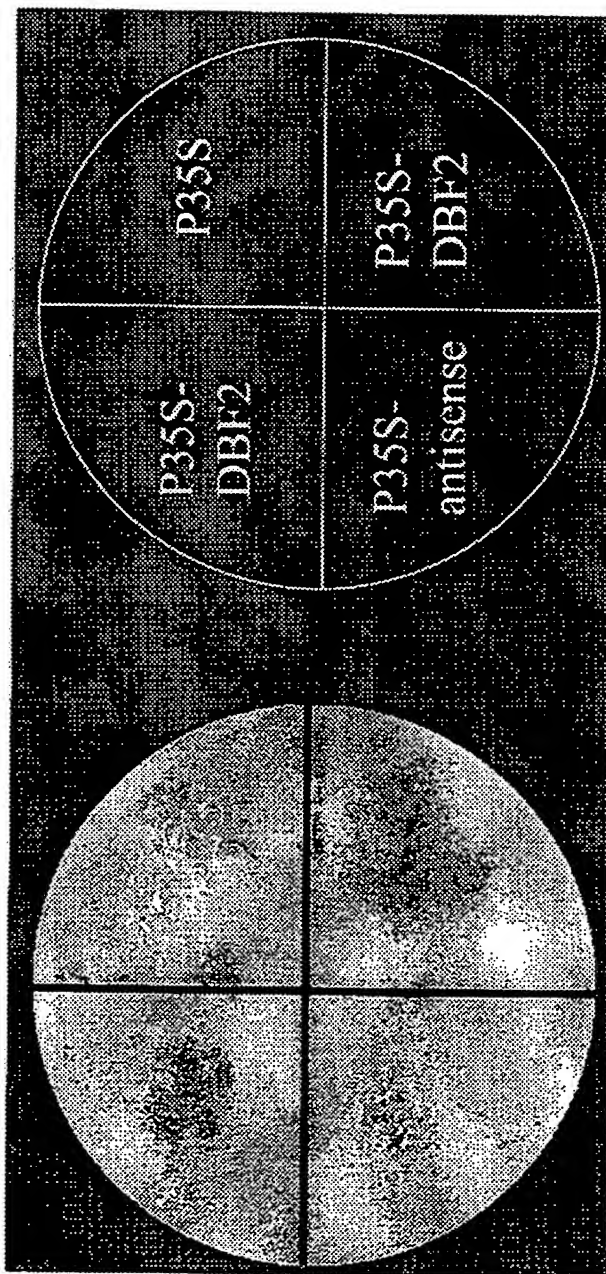


FIGURE 9

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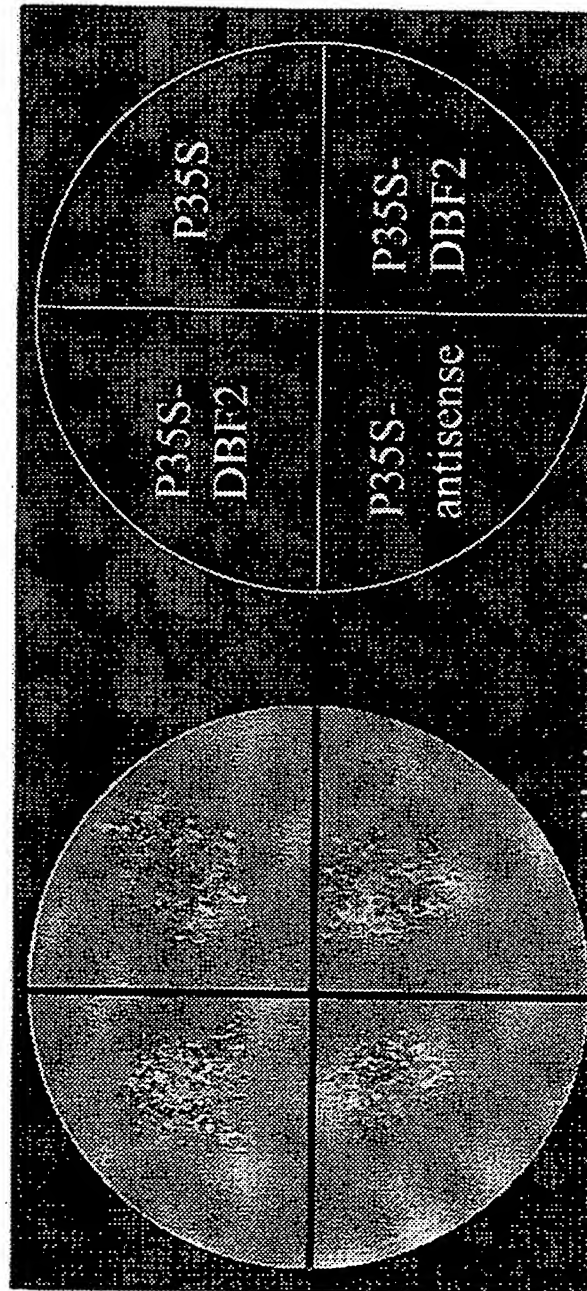


FIGURE 10

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FIGURE 11

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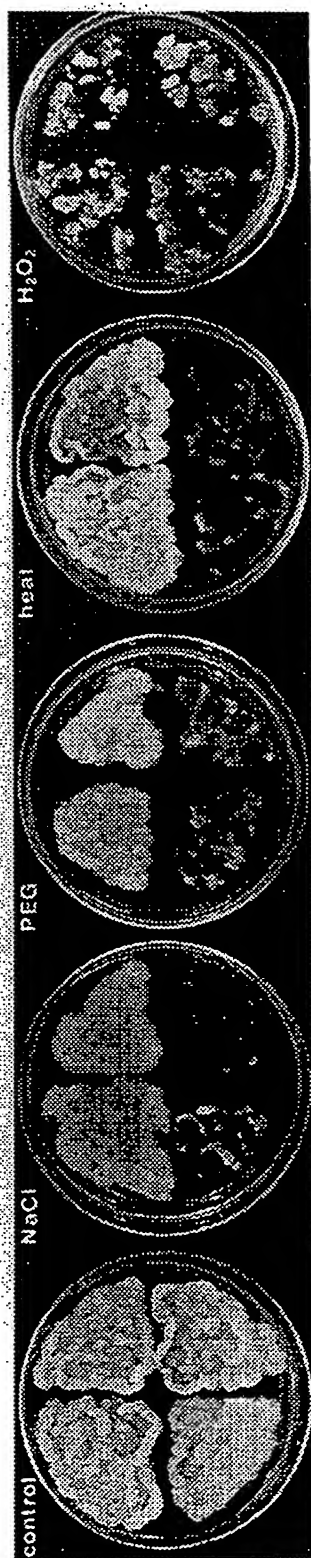


FIGURE 12A

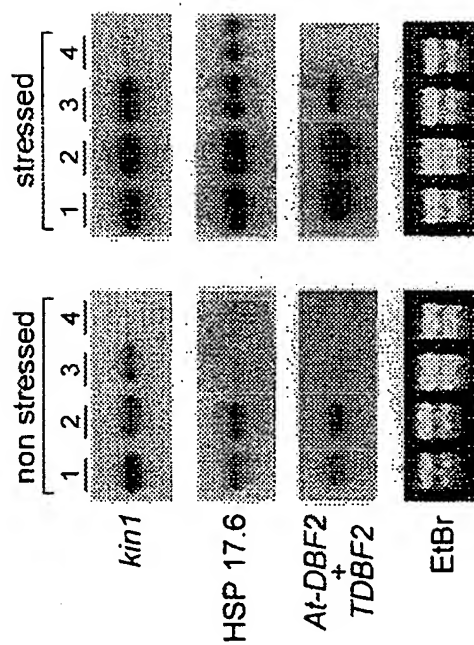


FIGURE 12c

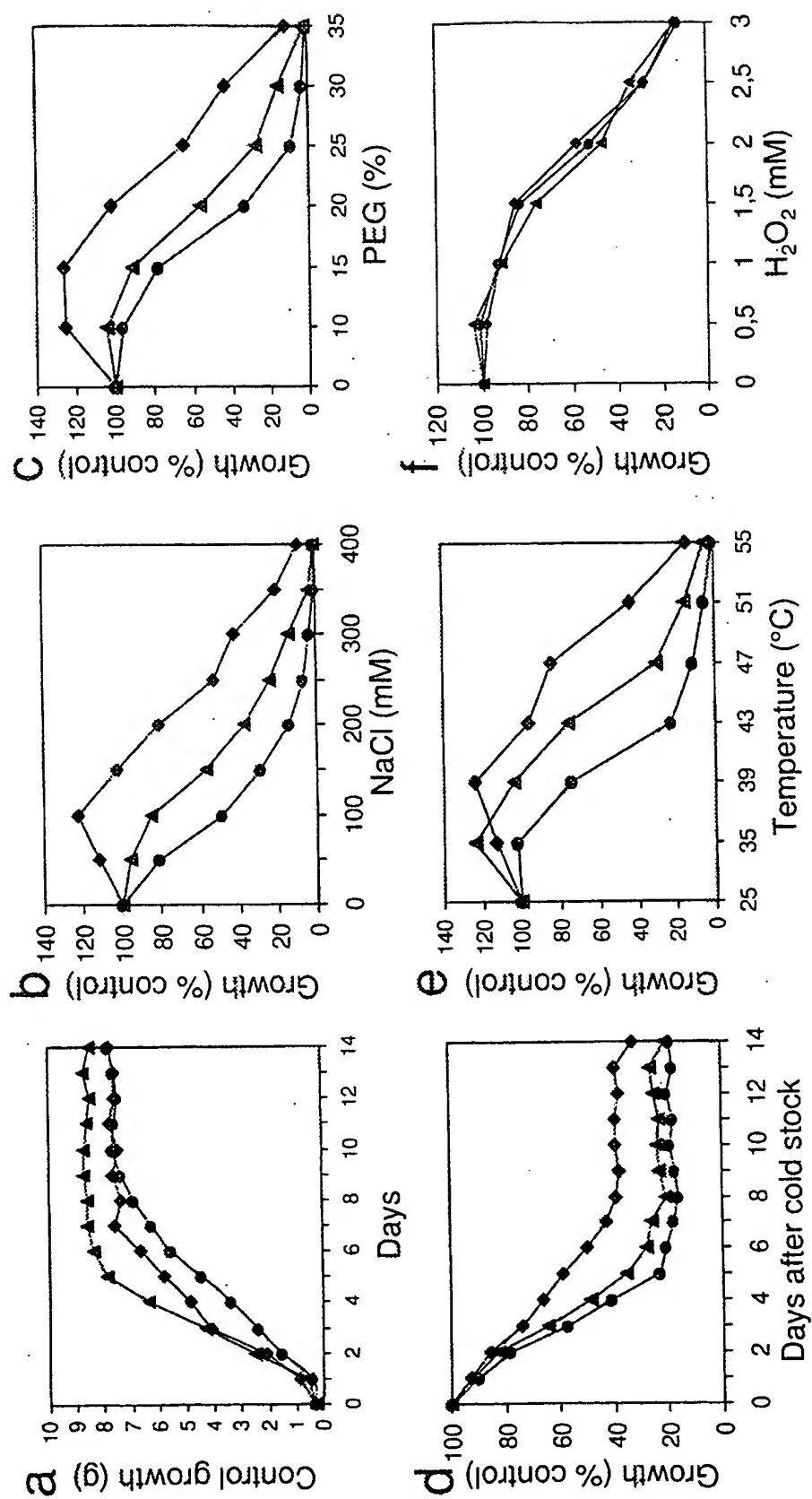


FIGURE 12B



FIGURE 13

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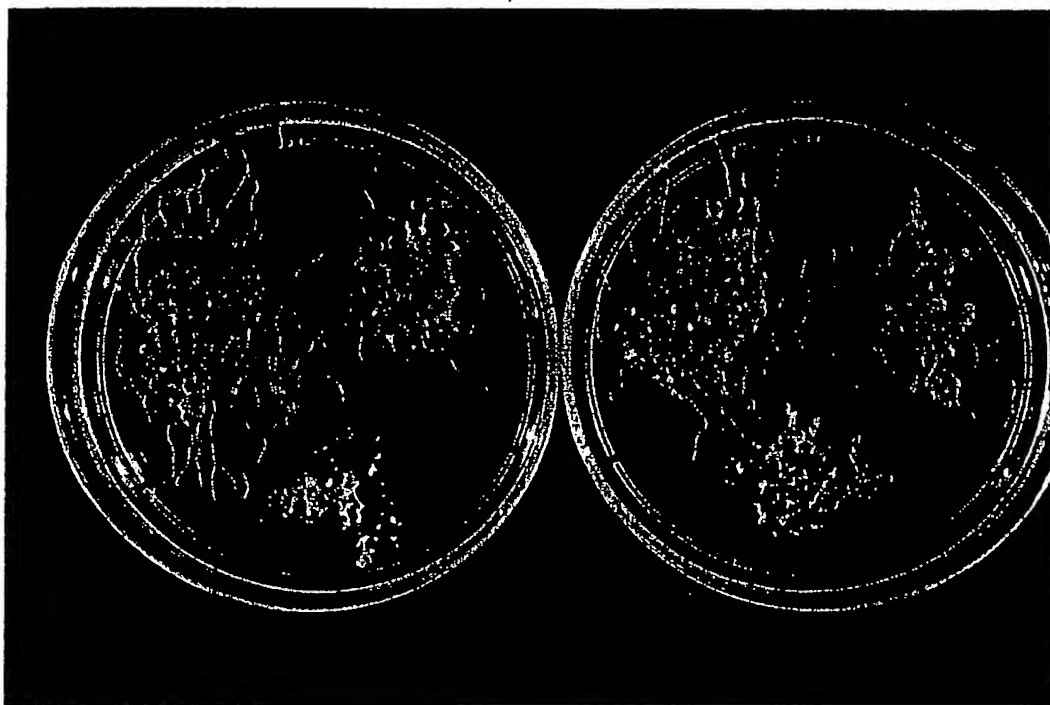


FIGURE 14

## SEQUENCE LISTING

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<120> Genes involved in tolerance to environmental stress

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 Ser Trp Lys Gln Thr Leu Asn Arg Ala Arg His Glu Asp Gly Arg Ala  
 385                                  390                                  395                                  400  
 Ala Phe Tyr Asn Arg Thr Trp Asp Leu Ile Thr Arg His Arg Ala Asp  
                                   405                                  410                                  415  
 Leu Ser Thr Arg Thr Arg Ser Phe Glu His Glu Val Lys Met Ser Tyr  
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 Phe Ala Asp Ile Leu Phe Lys Ala Leu Arg Ser Ile Ile Pro Pro Phe  
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 Thr Pro Gln Leu Asp Ser Glu Thr Asp Ala Gly Tyr Phe Asp Asp Phe  
                   450                                  455                                  460  
 Trp Asn Glu Ala Asp Ile Ala Lys Tyr Ala Asp Val Phe Asn Ser Gln  
 465                                  470                                  475                                  480  
 Cys Cys Arg Thr Ala Leu Val Asp Asp Ser Ala Val Ser Ser Lys Leu  
                                   485                                  490                                  495  
 Val Gly Phe Thr Phe Arg His Arg Asn Gly Lys Gln Gly Ser Ser Gly  
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&lt;400&gt; 3

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                               Met Asp Leu Glu Phe Gly Arg
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Phe Pro Ile Phe Ser Ile Leu Glu Asp Met Leu Glu Ala Pro Glu Glu
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caa acc gag aag act cgt aac aac cct tca aga gct tac atg cga gac 210
Gln Thr Glu Lys Thr Arg Asn Asn Pro Ser Arg Ala Tyr Met Arg Asp
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gca aag gca atg gct gct aca cca gct gac gtt atc gag cac ccg gat 258
Ala Lys Ala Met Ala Ala Thr Pro Ala Asp Val Ile Glu His Pro Asp
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gcg tac gtt ttc gcc gtg gac atg cct gga atc aaa gga gat gag att 306
Ala Tyr Val Phe Ala Val Asp Met Pro Gly Ile Lys Gly Asp Glu Ile
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cag gtc cag ata gag aac gag aac gtg ctt gtg gtg agt ggc aaa aga 354
Gln Val Gln Ile Glu Asn Glu Asn Val Leu Val Val Ser Gly Lys Arg
      75                               80                               85

cag agg gac aac aag gag aat gaa ggt gtg aag ttt gtg agg atg gag 402
Gln Arg Asp Asn Lys Glu Asn Glu Gly Val Lys Phe Val Arg Met Glu
      90                               95                               100

agg agg atg ggg aag ttt atg agg aag ttt cag tta cct gat aat gca 450
Arg Arg Met Gly Lys Phe Met Arg Lys Phe Gln Leu Pro Asp Asn Ala
      105                               110                               115

gat ttg gag aag atc tct gcg gct tgt aat gac ggt gtg ttg aaa gtg 498
Asp Leu Glu Lys Ile Ser Ala Ala Cys Asn Asp Gly Val Leu Lys Val
      120                               125                               130                               135

act att ccg aaa ctt cct cct cct gag cca aag aaa cca aag act ata 546
Thr Ile Pro Lys Leu Pro Pro Pro Glu Pro Lys Lys Pro Lys Thr Ile
      140                               145                               150

caa gtt caa gtc gct tga gtttgttgt gatccgtgtt tttgtgtttt 594
Gln Val Gln Val Ala
      155

aatgaatgta atcgataagc aactacctct tgggtgttcgt tgtaaatga aataaaaata 654

gttttctctg ttcataaaaa aaaaaaaaaa aaaactcgag c 695

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                           20                          25                          30  
 Ser Arg Ala Tyr Met Arg Asp Ala Lys Ala Met Ala Ala Thr Pro Ala  
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 Asp Val Ile Glu His Pro Asp Ala Tyr Val Phe Ala Val Asp Met Pro  
           50                          55                          60  
 Gly Ile Lys Gly Asp Glu Ile Gln Val Gln Ile Glu Asn Glu Asn Val  
           65                          70                          75                          80  
 Leu Val Val Ser Gly Lys Arg Gln Arg Asp Asn Lys Glu Asn Glu Gly  
                           85                          90                          95  
 Val Lys Phe Val Arg Met Glu Arg Arg Met Gly Lys Phe Met Arg Lys  
                           100                          105                          110  
 Phe Gln Leu Pro Asp Asn Ala Asp Leu Glu Lys Ile Ser Ala Ala Cys  
           115                          120                          125  
 Asn Asp Gly Val Leu Lys Val Thr Ile Pro Lys Leu Pro Pro Pro Glu  
           130                          135                          140  
 Pro Lys Lys Pro Lys Thr Ile Gln Val Gln Val Ala  
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 ttccaatcat cc atg agt ccg gac aat aaa ctg ctt ccg aag cgg atc atc 171  
                   Met Ser Pro Asp Asn Lys Leu Leu Pro Lys Arg Ile Ile  
                   1                          5                          10

ctt gta cgg cac ggt gaa tcg gaa ggg aat ctc gac acg gcg gcg tat	219
Leu Val Arg His Gly Glu Ser Glu Gly Asn Leu Asp Thr Ala Ala Tyr	
15 20 25	
aca acg acg ccg gat cat aag atc cag tta acg gat tcc ggt ttg ctt	267
Thr Thr Thr Pro Asp His Lys Ile Gln Leu Thr Asp Ser Gly Leu Leu	
30 35 40 45	
cag gcg cag gaa gcc gga gct cgt ctc cac gct ttg atc tct tct aat	315
Gln Ala Gln Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn	
50 55 60	
cct tct tca ccg gag tgg cgt gtg tac ttc tac gtt tcg ccg tac gat	363
Pro Ser Ser Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp	
65 70 75	
cgg act cga tct acg ctc cgg gag atc gga cgg tcg ttc tcg cgt cgc	411
Arg Thr Arg Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg	
80 85 90	
cgt gtg att ggt gtt cgc gaa gaa tgt cgg att agg gaa cag gat ttt	459
Arg Val Ile Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe	
95 100 105	
ggg aat ttt cag gtt aaa gag cga atg aga gca acg aaa aag gtc aga	507
Gly Asn Phe Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg	
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gag aga ttt ggc cgc ttt ttt tac cgg ttc ccg gag gga gaa tcc gcc	555
Glu Arg Phe Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala	
130 135 140	
gcc gat gtc ttc gat cgc gtc tcc agt ttt ctc gag tct cta tgg aga	603
Ala Asp Val Phe Asp Arg Val Ser Ser Phe Leu Glu Ser Leu Trp Arg	
145 150 155	
gac att gac atg aac aga ctg cac atc aac ccg tct cat gag cta aac	651
Asp Ile Asp Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn	
160 165 170	
ttt gtg att gtc tca cat ggc tta aca tcg cgt gtg ttt ctg atg aaa	699
Phe Val Ile Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys	
175 180 185	
tgg ttt aag tgg tca gtg gaa cag ttc gag gga cta aac aat cca ggg	747
Trp Phe Lys Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly	
190 195 200 205	
aac agt gag atc aga gtg atg gaa tta gga caa ggc ggt gat tac agc	795
Asn Ser Glu Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser	
210 215 220	
ttg gcg att cat cac aca gag gaa gag tta gcc aca tgg gga ctg tca	843
Leu Ala Ile His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser	
225 230 235	
cca gag atg att gca gat caa aag tgg cgg gct aac gcg cat aaa ggc	891

Pro Glu Met Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly  
 240 245 250

gaa tgg aaa gaa gat tgt aag tgg tat ttt ggt gat ttc ttc gac cat 939  
 Glu Trp Lys Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His  
 255 260 265

atg gca gat tcc gat aaa gag tgc gag act gag gcc act gaa gat aga 987  
 Met Ala Asp Ser Asp Lys Glu Cys Glu Thr Glu Ala Thr Glu Asp Arg  
 270 275 280 285

gaa gaa gaa gaa gaa gaa gag ggg aaa agg gta aat ctg cta acg agt 1035  
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 290 295 300

tca gaa tat agc aat gag cca gag tta tac aat gga caa tgc tgc tga 1083  
 Ser Glu Tyr Ser Asn Glu Pro Glu Leu Tyr Asn Gly Gln Cys Cys  
 305 310 315

tactatttta cagaacaaaa gcatacatga gaagaaacgt ttaactaaag aattcagaag 1143

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 35 40 45

Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn Pro Ser Ser  
 50 55 60

Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp Arg Thr Arg  
 65 70 75 80

Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg Arg Val Ile  
 85 90 95

Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe Gly Asn Phe  
 100 105 110

Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg Glu Arg Phe  
 115 120 125

Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala Ala Asp Val  
 130 135 140  
 Phe Asp Arg Val Ser Ser Phe Leu Glu Ser Leu Trp Arg Asp Ile Asp  
 145 150 155 160  
 Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn Phe Val Ile  
 165 170 175  
 Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys Trp Phe Lys  
 180 185 190  
 Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly Asn Ser Glu  
 195 200 205  
 Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser Leu Ala Ile  
 210 215 220  
 His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser Pro Glu Met  
 225 230 235 240  
 Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly Glu Trp Lys  
 245 250 255  
 Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His Met Ala Asp  
 260 265 270  
 Ser Asp Lys Glu Cys Glu Thr Glu Ala Thr Glu Asp Arg Glu Glu Glu  
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 Val Ala Ile Ile Thr Gly Gly Ala Arg Gly Ile Gly Ala Ala Thr Ala  
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Arg Leu Phe Thr Glu Asn Gly Ala Tyr Val Ile Val Ala Asp Ile Leu
      30                      35                      40

gat aat gaa ggc atc ctt gtg gcg gaa tcg atc ggt ggg tgt tac gtt 195
Asp Asn Glu Gly Ile Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val
      45                      50                      55

cat tgt gac gta tcg aag gag gct gat gtt gag gcg gca gtg gag cta 243
His Cys Asp Val Ser Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu
      60                      65                      70                      75

gca atg aga cgt aaa ggt aga cta gat gtg atg ttc aac aat gcc ggg 291
Ala Met Arg Arg Lys Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly
      80                      85                      90

atg tcg ctt aac gaa ggt agt atc atg ggg atg gac gtg gac atg gtt 339
Met Ser Leu Asn Glu Gly Ser Ile Met Gly Met Asp Val Asp Met Val
      95                      100                      105

aac aaa ctt gtc tcg gtt aat gtc aat ggt gtt ttg cat ggt atc aaa 387
Asn Lys Leu Val Ser Val Asn Val Asn Gly Val Leu His Gly Ile Lys
      110                      115                      120

cat gcc gct aag gcc atg atc aaa ggg gga cga gga ggc tcg ata ata 435
His Ala Ala Lys Ala Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile
      125                      130                      135

tgc aca tcg agc tca tca ggg cta atg gga gga ctt gga gga cat gcg 483
Cys Thr Ser Ser Ser Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala
      140                      145                      150                      155

tat acg ctc tcc aaa gga ggc atc aac ggg gtg gtg agg aca acg gag 531
Tyr Thr Leu Ser Lys Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu
      160                      165                      170

tgc gag ctt ggg tct cac ggc atc cgt gtg aat agc atc tct cct cat 579
Cys Glu Leu Gly Ser His Gly Ile Arg Val Asn Ser Ile Ser Pro His
      175                      180                      185

gga gtt ccc act gac atc ttg gtt aat gcg tac cgt aag ttc ctt aac 627
Gly Val Pro Thr Asp Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn
      190                      195                      200

aat gac aaa ctc aac gtc gct gag gtc acc gac att att gct gag aaa 675
Asn Asp Lys Leu Asn Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys
      205                      210                      215

ggg agt ttg ctg acc gga aga gcc ggt act gtg gag gac gta gct caa 723
Gly Ser Leu Leu Thr Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln
      220                      225                      230                      235

gca gct ttg ttt ctt gca agc caa gaa tcg tcg ggg ttc att acc gga 771
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cat aac ttg gtt gtt gat ggt ggt tac aca tct gcc act agt act atg 819

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His Asn Leu Val Val Asp Gly Gly Tyr Thr Ser Ala Thr Ser Thr Met  
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Arg Phe Ile Tyr Asn

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 35 40 45

Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val His Cys Asp Val Ser  
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Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu Ala Met Arg Arg Lys  
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Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly Met Ser Leu Asn Glu  
 85 90 95

Gly Ser Ile Met Gly Met Asp Val Asp Met Val Asn Lys Leu Val Ser  
 100 105 110

Val Asn Val Asn Gly Val Leu His Gly Ile Lys His Ala Ala Lys Ala  
 115 120 125

Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile Cys Thr Ser Ser Ser  
 130 135 140

Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala Tyr Thr Leu Ser Lys  
 145 150 155 160

Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu Cys Glu Leu Gly Ser  
 165 170 175

His Gly Ile Arg Val Asn Ser Ile Ser Pro His Gly Val Pro Thr Asp  
 180 185 190

Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn Asn Asp Lys Leu Asn  
 195 200 205

Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys Gly Ser Leu Leu Thr  
 210 215 220

Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln Ala Ala Leu Phe Leu

225		230		235		240									
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				245					250					255	
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 caaaatactt tttatgctca aaaacttact taaattctgt gatcgcttga acctaagtgg 234  
 atgatgtgga ttctctgttt tggctgccta tctttaagta aaacgtttta cccactgcgt 294  
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  Tyr Arg Pro Ser Ser Ala Tyr Asn Ala Pro Phe Tyr Thr Thr Asn
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ggg ggt gct cca gtc tcc aac aac atc tct tcc ctc acc atc gga gaa 1050
Gly Gly Ala Pro Val Ser Asn Asn Ile Ser Ser Leu Thr Ile Gly Glu
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cgtgatgtga ttatttttaa catgtgttac ttcgtaatgg gcag gt ccg gtt ctt 1219
                ly Pro Val Leu
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ctt gag gat tat cat ttg atc gag aag gtt gct aat ttc acc aga gag 1267
Leu Glu Asp Tyr His Leu Ile Glu Lys Val Ala Asn Phe Thr Arg Glu
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agg atc cct gag aga gtg gtt cat gct aga gga atc agt gct aag ggt 1315
Arg Ile Pro Glu Arg Val Val His Ala Arg Gly Ile Ser Ala Lys Gly
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Phe Phe Glu Val Thr His Asp Ile Ser Asn Leu Thr Cys Ala Asp Phe
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ctc aga gcc cct ggt gtt caa act ccg gtt att gtc cgt ttc tca acg 1411
Leu Arg Ala Pro Gly Val Gln Thr Pro Val Ile Val Arg Phe Ser Thr
                90                95                100                105

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Val Val His Gly Arg Ala Ser Pro Glu Thr Met Arg Asp Ile Arg Gly
                110                115                120

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ttt gct gtc aag ttt tac acc aga gag gtataagaaa gattcaaagt 1506  
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 gttatgatca g gga aac ttt gat ctt gtt ggg aac aac act ccg gtg ttc 1616  
 Gly Asn Phe Asp Leu Val Gly Asn Asn Thr Pro Val Phe  
 135 140

ttc atc cgt gat ggg att cag ttc ccg gat gtt gtc cac gcg ttg aaa 1664  
 Phe Ile Arg Asp Gly Ile Gln Phe Pro Asp Val Val His Ala Leu Lys  
 145 150 155

cct aac cga aaa aca aac atc caa gag tac tgg agg att ctg gac tac 1712  
 Pro Asn Arg Lys Thr Asn Ile Gln Glu Tyr Trp Arg Ile Leu Asp Tyr  
 160 165 170 175

atg tcc cac ttg cct gag agt ttg ctc aca tgg tgc tgg atg ttt gat 1760  
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 180 185 190

gat gtt ggt att cca caa gat tac agg cat atg gag ggt ttc ggt gtc 1808  
 Asp Val Gly Ile Pro Gln Asp Tyr Arg His Met Glu Gly Phe Gly Val  
 195 200 205

cac acc tac act ctt att gcc aaa tct gga aaa gtt ctc ttt gtg aag 1856  
 His Thr Tyr Thr Leu Ile Ala Lys Ser Gly Lys Val Leu Phe Val Lys  
 210 215 220

ttc cac tgg aaa cca act tgt ggg atc aag aat ctg act gat gaa gag 1904  
 Phe His Trp Lys Pro Thr Cys Gly Ile Lys Asn Leu Thr Asp Glu Glu  
 225 230 235

gcc aag gtt gtt gga gga gcc aat cac agc cac gcc act aag gat ctc 1952  
 Ala Lys Val Val Gly Gly Ala Asn His Ser His Ala Thr Lys Asp Leu  
 240 245 250 255

cac gat gcc att gca tct ggc aac tac ccc gag tgg aaa ctt ttc atc 2000  
 His Asp Ala Ile Ala Ser Gly Asn Tyr Pro Glu Trp Lys Leu Phe Ile  
 260 265 270

cag acc atg gat cct gca gat gag gat aag ttt gac ttt gac cca ctt 2048  
 Gln Thr Met Asp Pro Ala Asp Glu Asp Lys Phe Asp Phe Asp Pro Leu  
 275 280 285

gat gtg acc aag atc tgg cct gag gat att ttg cct ctg caa ccg gtt 2096  
 Asp Val Thr Lys Ile Trp Pro Glu Asp Ile Leu Pro Leu Gln Pro Val  
 290 295 300

ggt cgc ttg gtt ctg aac agg acc att gac aac ttc ttc aat gaa act 2144  
 Gly Arg Leu Val Leu Asn Arg Thr Ile Asp Asn Phe Phe Asn Glu Thr  
 305 310 315

gag cag ctt gcg ttc aac ccg ggt ctt gtg gtt cct gga atc tac tac 2192  
 Glu Gln Leu Ala Phe Asn Pro Gly Leu Val Val Pro Gly Ile Tyr Tyr

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320                               325                               330                               335
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cag aga cat cgc ctt gga ccg aat tat ttg cag ctt cca gtc aat gct 2288
Gln Arg His Arg Leu Gly Pro Asn Tyr Leu Gln Leu Pro Val Asn Ala
                               355                               360                               365

ccc aaa tgt gct cac cac aac aat cac cat gaa ggt ttt atg aac ttc 2336
Pro Lys Cys Ala His His Asn Asn His His Glu Gly Phe Met Asn Phe
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atg cac aga gat gag gag gtacgtctta gtacaccact tgagctacca 2384
Met His Arg Asp Glu Glu
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Glu Gln Leu Ala Phe Asn Pro Gly Leu Val Val Pro Gly Ile Tyr Tyr	325	330	335
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Asp Lys Pro Asn Lys Thr Leu Ser Ile Ile Asp Ser Gly Ile Gly Met
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acc aaa gca ggtaacgaat caatgcctaa taatctctcg ttggtgagat 701
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ggttatccat gattatttac tgttttgta c c agg gaa ctg ctg aaa gga gaa 1903  
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tca gag ggc ttg ttg aaa ctt cca act gac aag acc tta ttg gaa gac 1951  
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Ser Ala Thr Tyr Val Gly Val Tyr Asp Gly His Gly Gly Pro Glu Ala
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Ser Leu Pro Met Lys Pro Gln Met Ala Thr Val Gly Ser Cys Cys Leu
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Gly Ile Ala Arg Arg Leu Val Arg Ala Ala Leu Glu Glu			
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Lys Gly Ile Arg Arg His Phe His Asp Asp Ile Ser Val Ile Val Val			
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 Ser Gly Leu Lys Glu Ser Lys Gly Asn Lys Lys Ser Lys Glu Pro Tyr  
                                  210                      215                      220  
 Gly Lys Lys Arg Pro Met Glu Ser Ser Thr Tyr Ser Leu Ile Asp Asp  
                                  225                      230                      235                      240  
 Asp Asp Asp Asp Asp Asp Asp Asp Asp Asn Asp Thr Ser Gly His Glu  
                                  245                      250                      255  
 Thr Pro Arg Glu Trp Ser Trp Glu Lys Ser Pro Ser Gln Ser Ser Arg  
                                  260                      265                      270  
 Arg Arg Lys Lys Ser Glu Asp Thr Val Ile Asn Val Asp Glu Glu Glu  
                                  275                      280                      285  
 Ala Gln Pro Ser Thr Val Ala Glu Gln Ala Ala Glu Leu Pro Glu Gly  
                                  290                      295                      300  
 Leu Ile Lys Leu Gln Leu Ala Ile Tyr Lys Leu Ile Val Asp Lys Thr  
                                  305                      310                      315                      320  
 Cys Ser Leu Gln Glu Asp Ile Cys Tyr Pro Thr ArSeg Phe Leu Gln  
                                  325                      330                      e                      335  
 Gln Gln Ile Ser Sr Ser Asn Gln Ile Ser Ala Asp Cys His Phe Phe  
                                  340e                      345                      350  
 Asn Thr Tyr Phe Tr Lys Lys Leu Ser Asp Ala Val Thr Tyr Lys Gly  
                                  355y                      360                      365  
 Asn Asp Lys Ap Ala Phe Phe Val Arg Phe Arg Arg Trp Trp Lys Gly  
                                  370                      375                      380  
 Ile Asp Leu Pe Arg Lys Ala Tyr Ile Phe Ile Pro Ile His Glu r  
                                  385                      390                      395u  
 Leu His Trp Ser Leu Val Ile Val Cys Ile Pro Asp Lys Lys Asp Glu  
                                  400                      405                      410  
 Ser Gly Leu Thr Ile Leu His Leu Asp Ser Leu Gly Leu His Ser Arg  
                                  415                      420                      425  
 Lys Ser Ile Val Glu Asn Val Lys Arg Phe Leu Lys Asp Glu Trp Asn  
                                  430                      435                      440  
 Tyr Leu Asn Gln Asp Asp Tyr Ser Leu Asp Leu Pro Ile Ser Glu Lys

[illegible]

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<222> (22)..(1107)
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[illegible]

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 Val His Val Ser Asp Glu Ile Tyr Ser Asn Gly Gly Val Val Leu Pro  
                   335                  340                  345

cac aag gag atc aaa tca aac atc ttg aag cca gag ata gtg atg tga 1107  
 His Lys Glu Ile Lys Ser Asn Ile Leu Lys Pro Glu Ile Val Met  
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aa 1109

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<212> PRT

<213> Arabidopsis thaliana

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Leu Thr Leu Ser Phe Pro Lys Pro Leu Val Asp Phe Ala Asn Lys Pro  
                   20                  25                  30

Met Ile Leu His Gln Ile Glu Ala Leu Lys Ala Val Gly Val Asp Glu  
                   35                  40                  45

Val Val Leu Ala Ile Asn Tyr Gln Pro Glu Val Met Leu Asn Phe Leu  
                   50                  55                  60

Lys Asp Phe Glu Thr Lys Leu Glu Ile Lys Ile Thr Cys Ser Gln Glu  
                   65                  70                  75                  80

Thr Glu Pro Leu Gly Thr Ala Gly Pro Leu Ala Leu Ala Arg Asp Lys  
                   85                  90                  95

Leu Leu Asp Gly Ser Gly Glu Pro Phe Phe Val Leu Asn Ser Asp Val  
                   100                  105                  110

Ile Ser Glu Tyr Pro Leu Lys Glu Met Leu Glu Phe His Lys Ser His  
                   115                  120                  125

Gly Gly Glu Ala Ser Ile Met Val Thr Lys Val Asp Glu Pro Ser Lys  
                   130                  135                  140

Tyr Gly Val Val Val Met Glu Glu Ser Thr Gly Arg Val Glu Lys Phe  
                   145                  150                  155                  160

Val Glu Lys Pro Lys Leu Tyr Val Gly Asn Lys Ile Asn Ala Gly Ile  
                   165                  170                  175

Tyr Leu Leu Asn Pro Ser Val Leu Asp Lys Ile Glu Leu Arg Pro Thr  
                   180                  185                  190

Ser Ile Glu Lys Glu Thr Phe Pro Lys Ile Ala Ala Ala Gln Gly Leu  
                   195                  200                  205

Tyr Ala Met Val Leu Pro Gly Phe Trp Met Asp Ile Gly Gln Pro Arg  
 210 215 220  
 Asp Tyr Ile Thr Gly Leu Arg Leu Tyr Leu Asp Ser Leu Arg Lys Lys  
 225 230 235 240  
 Ser Pro Ala Lys Leu Thr Ser Gly Pro His Ile Val Gly Asn Val Leu  
 245 250 255  
 Val Asp Glu Thr Ala Thr Ile Gly Glu Gly Cys Leu Ile Gly Pro Asp  
 260 265 270  
 Val Ala Ile Gly Pro Gly Cys Ile Val Glu Ser Gly Val Arg Leu Ser  
 275 280 285  
 Arg Cys Thr Val Met Arg Gly Val Arg Ile Lys Lys His Ala Cys Ile  
 290 295 300  
 Ser Ser Ser Ile Ile Gly Trp His Ser Thr Val Gly Gln Trp Ala Arg  
 305 310 315 320  
 Ile Glu Asn Met Thr Ile Leu Gly Glu Asp Val His Val Ser Asp Glu  
 325 330 335  
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 cct tat cga acc aac tct tct ttc ggc tca aag tca tcg ctt ctc ttt 98  
 Pro Tyr Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe  
 15 20 25 30  
 cgg tct cca tcc tcc tcc tcc tca gtc tct atg acg aca acg cgt gga 146  
 Arg Ser Pro Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly  
 35 40 45  
 aac gtg gct gtg gcg gct gct gct aca tcc act gag gcg cta aga aaa 194  
 Asn Val Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys  
 50 55 60

gga ata gcg gag ttc tac aat gaa act tcg ggt ttg tgg gaa gag att	242
Gly Ile Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile	
65 70 75	
tgg gga gat cat atg cat cat ggc ttt tat gac cct gat tct tct gtt	290
Trp Gly Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val	
80 85 90	
caa ctt tct gat tct ggt cac aag gaa gct cag atc cgt atg att gaa	338
Gln Leu Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu	
95 100 105 110	
gag tct ctc cgt ttc gcc ggt gtt act gat gaa gag gag gag aaa aag	386
Glu Ser Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys	
115 120 125	
ata aag aaa gta gtg gat gtt ggg tgt ggg att gga gga agc tca aga	434
Ile Lys Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg	
130 135 140	
tat ctt gcc tct aaa ttt gga gct gaa tgc att ggc att act ctc agc	482
Tyr Leu Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser	
145 150 155	
cct gtt cag gcc aag aga gcc aat gat ctc gcg gct gct caa tca ctc	530
Pro Val Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu	
160 165 170	
tct cat aag gct tcc ttc caa gtt gcg gat gcg ttg gat cag cca ttc	578
Ser His Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe	
175 180 185 190	
gaa gat gga aaa ttc gat cta gtg tgg tcg atg gag agt ggt gag cat	626
Glu Asp Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His	
195 200 205	
atg cct gac aag gcc aag ttt gta aaa gag ttg gta cgt gtg gcg gct	674
Met Pro Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala	
210 215 220	
cca gga ggt agg ata ata ata gtg aca tgg tgc cat aga aat cta tct	722
Pro Gly Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser	
225 230 235	
gcg ggg gag gaa gct ttg cag ccg tgg gag caa aac atc ttg gac aaa	770
Ala Gly Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys	
240 245 250	
atc tgt aag acg ttc tat ctc ccg gct tgg tgc tcc acc gat gat tat	818
Ile Cys Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr	
255 260 265 270	
gtc aac ttg ctt caa tcc cat tct ctc cag gat att aag tgt gcg gat	866
Val Asn Leu Leu Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp	
275 280 285	

tgg tca gag aac gta gct cct ttc tgg cct gcg gtt ata cgg act gca 914  
 Trp Ser Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala  
 290 295 300  
 tta aca tgg aag ggc ctt gtg tct ctg ctt cgt agt ggt atg aaa agt 962  
 Leu Thr Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser  
 305 310 315  
 att aaa gga gca ttg aca atg cca ttg atg att gaa ggt tac aag aaa 1010  
 Ile Lys Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys  
 320 325 330  
 ggt gtc att aag ttt ggt atc atc act tgc cag aag cca ctc taa 1055  
 Gly Val Ile Lys Phe Gly Ile Ile Thr Cys Gln Lys Pro Leu  
 335 340 345  
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 <213> Arabidopsis thaliana

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 Pro Ser Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly Asn Val  
 35 40 45  
 Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys Gly Ile  
 50 55 60  
 Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile Trp Gly  
 65 70 75 80  
 Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val Gln Leu  
 85 90 95  
 Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu Glu Ser  
 100 105 110  
 Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys Ile Lys  
 115 120 125  
 Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Tyr Leu  
 130 135 140  
 Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser Pro Val  
 145 150 155 160  
 Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu Ser His  
 165 170 175

Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe Glu Asp  
 180 185 190  
 Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His Met Pro  
 195 200 205  
 Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala Pro Gly  
 210 215 220  
 Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser Ala Gly  
 225 230 235 240  
 Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys Ile Cys  
 245 250 255  
 Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr Val Asn  
 260 265 270  
 Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp Trp Ser  
 275 280 285  
 Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala Leu Thr  
 290 295 300  
 Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser Ile Lys  
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 ctc gag atc gac gat gac cag aaa cta cgt gcg ttt tac gac aag aga 95  
 Leu Glu Ile Asp Asp Asp Gln Lys Leu Arg Ala Phe Tyr Asp Lys Arg  
 20 25 30  
 atc tct caa gaa gtc agt gga gat gct ttg ggc gag gag ttc aaa gga 143  
 Ile Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly  
 35 40 45

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tac gtt ttc aag atc aag ggt ggt tgc gat aag caa ggt ttc cca atg 191
Tyr Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met
      50                      55                      60

aag cag gga gtt ttg act cca ggc cgt gtt cgc ctt ttg ctt cac cga 239
Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg
      65                      70                      75

gga act cct tgc ttc aga gga cat gga agg aga act ggt gag agg aga 287
Gly Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg
      80                      85                      90                      95

aga aag tct gtt cgt ggt tgc att gtg agc cct gat ctc tct gtt ctg 335
Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu
      100                      105                      110

aac ctt gtc att gtg aag aag ggt gag aac gat ctt cct ggg ctt acc 383
Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr
      115                      120                      125

gat cat gag agc aag atg aga gga cca aag aga gcc tcc aag atc cgt 431
Asp His Lys Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg
      130                      135                      140

aaa ctg ttt aac ctc aag aag gaa gat gat gtc agg acc tat gtc aac 479
Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn
      145                      150                      155

act tac cgc cgc aag ttc aca aac aag aag ggc aag gaa gtt agc aaa 527
Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys
      160                      165                      170                      175

gcc cct aag atc cag agg ctt gtg acc cca ttg act ctt cag agg aag 575
Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys
      180                      185                      190

aga gct aga att gct gac aag aag aag aaa att gct aag gct aat tct 623
Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser
      195                      200                      205

gat gct gct gat tac cag aag ctt ctc gcc tcg agg ttg aag gaa cag 671
Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln
      210                      215                      220

cgt gac agg agg agt gag agt ttg gca aaa gag agg tcg aga ctc tct 719
Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser
      225                      230                      235

tct gct gct gcc aag ccc tct gtc aca gct taa aaaagcttga gattca 768
Ser Ala Ala Ala Lys Pro Ser Val Thr Ala
      240                      245                      250

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&lt;210&gt; 28

&lt;211&gt; 249

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 28

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 Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly Tyr  
 35 40 45  
 Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met Lys  
 50 55 60  
 Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly  
 65 70 75 80  
 Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg Arg  
 85 90 95  
 Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn  
 100 105 110  
 Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp  
 115 120 125  
 His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys  
 130 135 140  
 Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn Thr  
 145 150 155 160  
 Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys Ala  
 165 170 175  
 Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys Arg  
 180 185 190  
 Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser Asp  
 195 200 205  
 Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln Arg  
 210 215 220  
 Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser Ser  
 225 230 235 240  
 Ala Ala Ala Lys Pro Ser Val Thr Ala  
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&lt;211&gt; 1201

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

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ctcttctctt ttctctgtca ctaattttca g act gag aaa gct ttt ctt aag 167  
 Thr Glu Lys Ala Phe Leu Lys  
 5 10

cag cct aag gtc ttc ctt ag gtaattttgc gattcgattt ctctctgttc 217  
 Gln Pro Lys Val Phe Leu Se  
 15

tctattgttt cattgtattt aagttccaag ttgtttatat tgttcattgt ttctgattta 277

tcaag c tcg aag aaa tct gga aag gga aag aga cct gga aaa ggt gga 325  
 r Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly  
 20 25 30

aac cgt ttc tgg aag aac att ggt ttg ggc ttc aag act cct cgt gaa 373  
 Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu  
 35 40 45

gcc att gat g gtatgtttta gcttttaact cgttataata gataaggaac 423  
 Ala Ile Asp G  
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tcttggattg tggtgttcat atagtcgata gatttcaaatt gctattttgt cttgtagaat 483

cttaagcttt ggtttagtga gttctgatcc ttcagcttta tctggatcta cattactggt 543

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tcagtgatgc aaatgttatc agtagatttt gaattagtag gatgtcactg atttgaatat 603
gtgatcaagc ttcatagaaa cctgcatcat tctctatata cctttaagtc agattctcag 663
gttattgtgt atttgtgtgg aacag ga gct tac gtt gac aag aaa tgc ccc 714
                               ly Ala Tyr Val Asp Lys Lys Cys Pro
                               55                               60
ttc act gga act gtt tcc att aga ggt cgt atc tta gct ggt act tgc 762
Phe Thr Gly Thr Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys
                               65                               70                               75
cac agt gcg aaa atg cag agg acc att atc gtg cga agg gat tac ctt 810
His Ser Ala Lys Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu
                               80                               85                               90
cac ttt gtg aag aag tat cag ag gtaaattcat acattctcat acttctttcc 863
His Phe Val Lys Lys Tyr Gln Ar
                               95
atagagtctt acacattgat gtttaagaaa gtaatatcct ttttgttctt ag g tat 919
                               g Tyr
                               100
gag aag agg cat tca aac att ccg gct cat gtc tca cca tgc ttc cgt 967
Glu Lys Arg His Ser Asn Ile Pro Ala His Val Ser Pro Cys Phe Arg
                               105                               110                               115
gtt aag gaa gga gac cat atc atc att ggc caa tgc ag gttatgatct 1015
Val Lys Glu Gly Asp His Ile Ile Ile Gly Gln Cys Ar
                               120                               125
gattcaaacc tacaaattgt ctccattgat tctgattatc gtgaatttgt tttgatcttt 1075
ttgtttgtta atgattgata atttcag g cca ttg tcg aag aca gtg agg ttc 1127
                               g Pro Leu Ser Lys Thr Val Arg Phe
                               130                               135
aat gtg ttg aag gtg ata cca gct ggg tct tct tct tca ttt gga aag 1175
Asn Val Leu Lys Val Ile Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys
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aag gca ttc act gga atg taa gctgc 1201
Lys Ala Phe Thr Gly Met
155                               160

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&lt;210&gt; 30

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 30

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  1           5           10           15

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                   35                  40                  45  
 Glu Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly  
                   50                  55                  60  
 Thr Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala  
                   65                  70                  75                  8  
 Lys Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu His Phe Val  
                   85                  90                  95  
 Lys Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His  
                   100                  105                  110  
 Val Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Ile Ile Ile Gly  
                   115                  120                  125  
 Gln Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys Val  
                   130                  135                  140  
 Ile Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys Lys Ala Phe Thr Gly  
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 ctc atc gaa gaa ggt tta att tta cag gaa gtg aaa ttg tat gct gaa 100  
 Leu Ile Glu Glu Gly Leu Ile Leu Gln Glu Val Lys Leu Tyr Ala Glu  
                                   15                  20                  25  
 gat ggt tca gtg gac ttt aat gga aac cca cca ttg aag gag aaa aca 148  
 Asp Gly Ser Val Asp Phe Asn Gly Asn Pro Pro Leu Lys Glu Lys Thr  
                                   30                  35                  40  
 gga aac tgg aaa gct tgt cct ttt att ctt ggt aat gaa tgt tgt gag 196  
 Gly Asn Trp Lys Ala Cys Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu  
                   45                  50                  55

agg cta gct tac tat ggt att gct ggg aat tta atc act tac ctc acc	244
Arg Leu Ala Tyr Tyr Gly Ile Ala Gly Asn Leu Ile Thr Tyr Leu Thr	
60 65 70	
act aag ctt cac caa gga aat gtt tct gct gct aca aac gtt acc aca	292
Thr Lys Leu His Gln Gly Asn Val Ser Ala Ala Thr Asn Val Thr Thr	
75 80 85 90	
tgg caa ggg act tgt tat ctc act cct ctc att gga gct gtt ctg gct	340
Trp Gln Gly Thr Cys Tyr Leu Thr Pro Leu Ile Gly Ala Val Leu Ala	
95 100 105	
gat gct tac tgg gga cgt tac tgg acc atc gct tgt ttc tcc ggg att	388
Asp Ala Tyr Trp Gly Arg Tyr Trp Thr Ile Ala Cys Phe Ser Gly Ile	
110 115 120	
tat ttc atc ggg atg tct gcg tta act ctt tca gct tca gtt ccg gca	436
Tyr Phe Ile Gly Met Ser Ala Leu Thr Leu Ser Ala Ser Val Pro Ala	
125 130 135	
ttg aag cca gcg gaa tgt att ggt gac ttt tgt cca tct gca acg cca	484
Leu Lys Pro Ala Glu Cys Ile Gly Asp Phe Cys Pro Ser Ala Thr Pro	
140 145 150	
gct cag tat gcg atg ttc ttt ggt ggg ctt tac ctg atc gct ctt gga	532
Ala Gln Tyr Ala Met Phe Phe Gly Gly Leu Tyr Leu Ile Ala Leu Gly	
155 160 165 170	
act gga ggt atc aaa ccg tgt gtc tca tcc ttc ggt gcc gat cag ttt	580
Thr Gly Gly Ile Lys Pro Cys Val Ser Ser Phe Gly Ala Asp Gln Phe	
175 180 185	
gat gac acg gac tct cgg gaa cga gtt aga aaa gct tcg ttc ttt aac	628
Asp Asp Thr Asp Ser Arg Glu Arg Val Arg Lys Ala Ser Phe Phe Asn	
190 195 200	
tgg ttt tac ttc tcc atc aat att gga gca ctt gtg tca tct agt ctt	676
Trp Phe Tyr Phe Ser Ile Asn Ile Gly Ala Leu Val Ser Ser Ser Leu	
205 210 215	
cta gtt tgg att caa gag aat cgg ggg tgg ggt tta ggg ttt ggg ata	724
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Pro Thr Val Phe Met Gly Leu Ala Ile Ala Ser Phe Phe Phe Gly Thr	
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Pro Leu Tyr Arg Phe Gln Lys Pro Gly Gly Ser Pro Ile Thr Arg Ile	
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Ser Gln Val Val Val Ala Ser Phe Arg Lys Ser Ser Val Lys Val Pro	
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Ala Gly Ser Arg Lys Ile	Glu His Thr Asp Asp Cys Gln Tyr Leu Asp	
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Lys Ala Ala Val Ile Ser	Glu Glu Glu Ser Lys Ser Gly Asp Tyr Ser	
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Leu Ile Arg Met Phe Pro Ile Trp	Ala Ser Gly Ile Ile Phe Ser Ala	
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gta tac gca caa atg tcc aca atg ttt gtt caa caa ggc cga gcc atg		1156
Val Tyr Ala Gln Met Ser Thr Met Phe Val Gln Gln Gly Arg Ala Met		
365	370	375
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Asn Cys Lys Ile Gly Ser Phe Gln Leu Pro Pro	Ala Ala Leu Gly Thr	
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ttc gac aca gca agc gtc atc atc tgg gtg ccg ctc tac gac cgg ttc		1252
Phe Asp Thr Ala Ser Val Ile Ile Trp	Val Pro Leu Tyr Asp Arg Phe	
395	400	405
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Ile Val Pro Leu Ala Arg Lys Phe Thr	Gly Val Asp Lys Gly Phe Thr	
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Glu Ile Gln Arg Met Gly Ile Gly Leu Phe Val Ser Val Leu Cys Met		
430	435	440
gca gct gca gct atc gtc gaa atc atc cgt ctc cat atg gcc aac gat		1396
Ala Ala Ala Ala Ile Val Glu Ile Ile Arg Leu His Met Ala Asn Asp		
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ctt gga tta gtc gag tca gga gcc cca gtt ccc ata tcc gtc ttg tgg		1444
Leu Gly Leu Val Glu Ser Gly Ala Pro Val Pro	Ile Ser Val Leu Trp	
460	465	470
cag att cca cag tac ttc att ctc ggt gca gcc gaa gta ttc tac ttc		1492
Gln Ile Pro Gln Tyr Phe Ile Leu Gly Ala Ala Glu Val Phe Tyr Phe		
475	480	485
atc ggt cag ctc gag ttc ttc tac gac caa tct cca gat gca atg aga		1540
Ile Gly Gln Leu Glu Phe Phe Tyr Asp	Gln Ser Pro Asp Ala Met Arg	
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Ser Leu Cys Ser Ala Leu Ala Leu Leu Thr	Asn Ala Leu Gly Asn Tyr	

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Gly Gln Glu Gly Trp Ile Ser Asp Asn Leu Asn Ser Gly His Leu Asp			
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Tyr Phe Phe Trp Leu Leu Ala Gly Leu Ser Leu Val Asn Met Ala Val			
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Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu Arg Leu Ala Tyr Tyr Gly	
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Ile Ala Gly Asn Leu Ile Thr Tyr Leu Thr Thr Lys Leu His Gln Gly	
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Tyr Trp Thr Ile Ala Cys Phe Ser Gly Ile Tyr Phe Ile Gly Met Ser	
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 Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr Asp Ser Arg  
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 Glu Arg Val Arg Lys Ala Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile  
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 225 230 235 240  
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 Ser Phe Arg Lys Ser Ser Val Lys Val Pro Glu Asp Ala Thr Leu Leu  
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 Glu His Thr Asp Asp Cys Gln Tyr Leu Asp Lys Ala Ala Val Ile Ser  
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 325 330 335  
 Thr Val Thr Gln Val Glu Glu Leu Lys Ile Leu Ile Arg Met Phe Pro  
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 Glu Ile Ile Arg Leu His Met Ala Asn Asp Leu Gly Leu Val Glu Ser  
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Gly Ala Pro Val Pro Ile Ser Val Leu Trp Gln Ile Pro Gln Tyr Phe  
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 Leu Val Phe Arg Ser Ser Leu Ala Gly Asp Asp Gly Thr Ser Gly Gly  
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 Gly Leu Ser Gly Phe Val Gly Lys Ile Asn Ser Ser Ile Arg Ser Ser  
 30 35 40  
 cga att ggg ctc ttt tct aag ccg cct cca ggg ctt cct gct cct aga 196  
 Arg Ile Gly Leu Phe Ser Lys Pro Pro Pro Gly Leu Pro Ala Pro Arg  
 45 50 55  
 aaa gaa gaa gcg ccg tcg att cgg tgg agg aaa ggg gaa tta atc ggt 244  
 Lys Glu Glu Ala Pro Ser Ile Arg Trp Arg Lys Gly Glu Leu Ile Gly  
 60 65 70 75  
 tgc ggt gct ttt gga aga gtt tac atg gga atg aac ctc gat tcc ggc 292

Cys	Gly	Ala	Phe	Gly	Arg	Val	Tyr	Met	Gly	Met	Asn	Leu	Asp	Ser	Gly		
				80					85					90			
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Glu	Leu	Leu	Ala	Ile	Lys	Gln	Val	Leu	Ile	Ala	Pro	Ser	Ser	Ala	Ser		
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Lys	Glu	Lys	Thr	Gln	Gly	His	Ile	Arg	Glu	Leu	Glu	Glu	Glu	Val	Gln		
		110					115					120					
ctt	ctt	aag	aat	ctt	tca	cat	ccg	aac	atc	gtt	aga	tac	ttg	ggc	act	436	
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Val	Arg	Glu	Ser	Asp	Ser	Leu	Asn	Ile	Leu	Met	Glu	Phe	Val	Pro	Gly		
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Gly	Ser	Ile	Ser	Ser	Leu	Leu	Glu	Lys	Phe	Gly	Ser	Phe	Pro	Glu	Pro		
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Val	Ile	Ile	Met	Tyr	Thr	Lys	Gln	Leu	Leu	Leu	Gly	Leu	Glu	Tyr	Leu		
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cac	aac	aat	ggg	atc	atg	cat	cga	gat	att	aag	ggg	gca	aat	att	ttg	628	
His	Asn	Asn	Gly	Ile	Met	His	Arg	Asp	Ile	Lys	Gly	Ala	Asn	Ile	Leu		
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gtc	gat	aac	aaa	ggc	tgc	atc	aga	ctc	gca	gat	ttt	ggc	gct	tcc	aag	676	
Val	Asp	Asn	Lys	Gly	Cys	Ile	Arg	Leu	Ala	Asp	Phe	Gly	Ala	Ser	Lys		
	205					210					215						
aaa	gtt	gta	gag	cta	gct	act	gta	aat	ggc	gcc	aaa	tct	atg	aag	ggg	724	
Lys	Val	Val	Glu	Leu	Ala	Thr	Val	Asn	Gly	Ala	Lys	Ser	Met	Lys	Gly		
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Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu	Val	Ile	Leu	Gln	Thr	Gly	His	Ser		
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Phe	Ser	Ala	Asp	Ile	Trp	Ser	Val	Gly	Cys	Thr	Val	Ile	Glu	Met	Ala		
			255					260					265				
acg	ggg	aag	cct	ccc	tgg	agc	gag	cag	tat	cag	cag	ttt	gct	gct	gtc	868	
Thr	Gly	Lys	Pro	Pro	Trp	Ser	Glu	Gln	Tyr	Gln	Gln	Phe	Ala	Ala	Val		
		270					275					280					
ctt	cat	att	ggc	aga	aca	aaa	gct	cat	cct	cca	att	cca	gaa	gac	ctc	916	
Leu	His	Ile	Gly	Arg	Thr	Lys	Ala	His	Pro	Pro	Ile	Pro	Glu	Asp	Leu		
		285				290					295						
tca	cca	gag	gct	aaa	gac	ttt	cta	atg	aaa	tgc	tta	cac	aaa	gaa	cca	964	
Ser	Pro	Glu	Ala	Lys	Asp	Phe	Leu	Met	Lys	Cys	Leu	His	Lys	Glu	Pro		

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agc ttg aga ctc tct gca acc gaa ttg ctt cag cac ccg ttt gtc act				1012
Ser Leu Arg Leu	Ser Ala Thr Glu Leu	Leu Gln His Pro Phe	Val Thr	
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Gly Lys Arg Gln Glu Pro Tyr Pro Ala Tyr Arg Asn Ser Leu Thr Glu				
	335	340	345	
tgt gga aac cca ata act act caa gga atg aat gtt cgg agt tca ata				1108
Cys Gly Asn Pro Ile Thr Thr Gln Gly Met Asn Val Arg Ser Ser Ile				
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Asn Ser Leu Ile Arg Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys				
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Glu Leu Gly Ser Leu Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn				
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aac tca gga ttt ggt tgg cga gat gga gac tct gat gac ctt tgt cag				1252
Asn Ser Gly Phe Gly Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln				
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Thr Asp Met Asp Asp Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val				
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Leu Ser Gln Ser Thr Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp				
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Ser Thr Asp Asn Trp Ser Cys Lys Phe Asp Glu Ser Pro Lys Val Met				
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aaa agc aaa tct aac ctg ctt tct tac caa gct tct caa ctc caa act				1444
Lys Ser Lys Ser Asn Leu Leu Ser Tyr Gln Ala Ser Gln Leu Gln Thr				
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gga gtt cca tgt gat gag gaa acc agc tta aca ttt gct ggt ggc tct				1492
Gly Val Pro Cys Asp Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser				
	480	485	490	
tcc gtt gca gag gat gat tat aaa ggc aca gag ttg aaa ata aaa tca				1540
Ser Val Ala Glu Asp Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser				
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Phe Leu Asp Glu Lys Ala Gln Asp Leu Lys Arg Leu Gln Thr Pro Leu				
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ctt gaa gaa ttc cac aat gct atg aat cca gga ata ccc caa ggt gca				1636
Leu Glu Glu Phe His Asn Ala Met Asn Pro Gly Ile Pro Gln Gly Ala				
	525	530	535	

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aag aca cct aaa cga ctt ccg agt aga cga ctc tca gca atc agt gat 1732
Lys Thr Pro Lys Arg Leu Pro Ser Arg Arg Leu Ser Ala Ile Ser Asp
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gct atg ccc agc cca ctc aaa agc tcc aaa cgt aca ctg aac aca agc 1780
Ala Met Pro Ser Pro Leu Lys Ser Ser Lys Arg Thr Leu Asn Thr Ser
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aga gtg atg cag tca gga act gaa cca act caa gtc aac gag tcg acc 1828
Arg Val Met Gln Ser Gly Thr Glu Pro Thr Gln Val Asn Glu Ser Thr
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tgg gaa gaa gaa ctc tat gaa gag ctt gag agg cat cga gag aat ctg 1924
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620          625          630          635

cga cac gct ggt gca gga ggg aag act cca tta tca ggc cac aaa gga 1972
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Ser Ile Arg Trp Arg Lys Gly Glu Leu Ile Gly Cys Gly Ala Phe Gly
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Arg Val Tyr Met Gly Met Asn Leu Asp Ser Gly Glu Leu Leu Ala Ile
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Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro	
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cca acg gca gat aca gtc gtg gcg gga agg acg agt tta ggt gag gcg	192
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cta agc atg aga ccg acg tcc tcg cca aca agg cga att gac cca caa	384
Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln	
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Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met	
130 135 140	
gcc acc tct cgc act gac gat acg cta ata gag gca gag acc ggt cgc	480
Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg	
145 150 155 160	
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Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala	
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aaa gac tac aag gag ggg gga att gcg gca tac ttt ggt tta cga gtg	576
Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val	
180 185 190	
ctg cga tgc tac tcg agg atc gta cga tcg atg aaa cgc cca ggc aac	624
Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn	
195 200 205	
ttg aaa ttc acg tgc cgg agg gat gtg gca ata gcc acg ttc agc ggc	672
Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly	

210	215	220	
aca ggc aga atg cag ctg agt atg aac agc cgt ttg cga gtc gag agc Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser 225 230 235 240			720
ctc gtg tcc gcg ggc cag agc gtg gcg tca ttc tgc ctt ttc ctg ata Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile 245 250 255			768
tgc acg gcg ccc tcg gcg atg cgg ctg gtt agc ctt ctt aca ctg acc Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr 260 265 270			816
cca agc atg acc tac cta aca tgc ggg ctg gga tgg atg acc gtc gtc Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val 275 280 285			864
gta ctg ccg gcg ata gtg gtc cac tgt tat atg cgc cga cat acg gaa Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu 290 295 300			912
ggg gga tgg cgg tat gcg gca ctc gag gag cat aag acg gag ccg gga Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly 305 310 315 320			960
cga aat gaa aag atc acc cgg agt aga cgc aac tcg gcg ttc ggc ggg Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly 325 330 335			1008
ctg gtc ggt cga aat aaa aga cga aag aag tcc aag gtc tcc ggg gca Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala 340 345 350			1056
ccg aca gcg gtt tac aca gcg atg ttt ttc atg ttc tcc acg gca atc Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile 355 360 365			1104
aag ggg atg gtg gtg tgc aca atg aaa aaa aaa gtc aaa aaa agt gcg Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala 370 375 380			1152
aat cgc aga ctc cgc cag ttg ctc cga tgg gcg cga tac cac gcg aac Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn 385 390 395 400			1200
gcg ttc ttg ctc tgt tct ctt gca tgc gca cga ttc gcg gca tcg cga Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg 405 410 415			1248
acg gtc atc cat tgc agt att tac cca cgt ttc ggc ccc tta gcc acg Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr 420 425 430			1296
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gag gca gac acg acg cga cac gaa aat gac gac gcc cgg aag gtg atg 1392
Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met
    450                455                460

gaa gac atg gcc aaa cga atg gac gat agt agc agt ggg agc acg ttg 1440
Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu
465                470                475                480

agc acg ctc acg act gac gag acg tac cac acc acc acg gag gtg acc 1488
Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr
    485                490                495

gat ttt gat tca tct cca tcg tgg gga cga tgc tca tcg cgg cgc ccg 1536
Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro
    500                505                510

ccg gcg ctg ctg gaa tcg aca ttt cgg cga tcc ccg aga ggg tcg acg 1584
Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr
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gga cga cga tgg cga gag tag attcggagtc aggaacgttg gaccgacagg 1635
Gly Arg Arg Trp Arg Glu
    530                535

tggaccgggtt tagggcagtt gacggtaggg gttgcctgac cagccttgac gctcgacagc 1695

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Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro
    35                40                45

Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala
    50                55                60

Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala
    65                70                75                80

Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg
    85                90                95

Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp
    100                105                110

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Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln  
 115 120 125  
 Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met  
 130 135 140  
 Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg  
 145 150 155 160  
 Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala  
 165 170 175  
 Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val  
 180 185 190  
 Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn  
 195 200 205  
 Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly  
 210 215 220  
 Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser  
 225 230 235 240  
 Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile  
 245 250 255  
 Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr  
 260 265 270  
 Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val  
 275 280 285  
 Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu  
 290 295 300  
 Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly  
 305 310 315 320  
 Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly  
 325 330 335  
 Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala  
 340 345 350  
 Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile  
 355 360 365  
 Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala  
 370 375 380  
 Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn  
 385 390 395 400  
 Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg  
 405 410 415

Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr  
 420 425 430  
 Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr  
 435 440 445  
 Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met  
 450 455 460  
 Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu  
 465 470 475 480  
 Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr  
 485 490 495  
 Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro  
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 Ala Lys Lys Gly Ala Asn Leu Phe Lys  
 15 20  
 ccgctgaaaa ttctcacggc gcattctatc ccgcagaact tttctgacca ctttgtag 155  
 acc cgc tgc gct cag tgc cac acc ctg aag gcc ggc gag ggc aac aag 203  
 Thr Arg Cys Ala Gln Cys His Thr Leu Lys Ala Gly Glu Gly Asn Lys  
 25 30 35

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att ggc cct gag ctc cac ggt ctc ttc ggc cgc aag act ggt tcc gtc 251
Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys Thr Gly Ser Val
      40              45              50

gct ggc tac tca tac acc gac gcc aac aag cag aag ggt atc gag tgg 299
Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys Gly Ile Glu Trp
      55              60              65

aag gac gac act ctc gtacgtcacg ccaccggaag attgaaatgt ccccgagacc 354
Lys Asp Asp Thr Leu
      70

ctccgctaac acgacacag ttc gag tac ctc gag aac ccc aag aag tac att 406
      Phe Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile
              75              80

ccc ggt acc aag atg gcc ttc ggt ggt ctc aag aag ccc aag gac cgc 454
Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys Pro Lys Asp Arg
      85              90              95              100

aac gac ctc atc acc ttc ctt gag gag gag acc aaa taa gcgtcttgc 503
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Glu Gly Asn Lys Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys
      35              40              45

Thr Gly Ser Val Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys
      50              55              60

Gly Ile Glu Trp Lys Asp Asp Thr Leu Phe Glu Tyr Leu Glu Asn Pro
      65              70              75              80

Lys Lys Tyr Ile Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys
      85              90              95

Pro Lys Asp Arg Asn Asp Leu Ile Thr Phe Leu Glu Glu Glu Thr Lys
      100              105              110

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 tta atc aga act cca caa aca aaa caa cgt ctc aat ttc cac tca aaa 96  
 Leu Ile Arg Thr Pro Gln Thr Lys Gln Arg Leu Asn Phe His Ser Lys  
                   20                  25                  30  
  
 acc cca aac cca gac gga tct aaa gat cca tct cca ccg gag cat cca 144  
 Thr Pro Asn Pro Asp Gly Ser Lys Asp Pro Ser Pro Pro Glu His Pro  
           35                  40                  45

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gtt gaa gta atc ggc cgg atc cga gat tac cct gac cgg aaa gag aaa 192
Val Glu Val Ile Gly Arg Ile Arg Asp Tyr Pro Asp Arg Lys Glu Lys
    50                55                60

tca cct tcg atc tta caa gtc aac aca gat aat caa acg gta cga gtc 240
Ser Pro Ser Ile Leu Gln Val Asn Thr Asp Asn Gln Thr Val Arg Val
    65                70                75                80

aga gct gat gtt ggg tac aga gac ttc aca ctc gac ggt gtt tct ttc 288
Arg Ala Asp Val Gly Tyr Arg Asp Phe Thr Leu Asp Gly Val Ser Phe
                85                90                95

tcg gag caa gaa ggt ctt gaa gag ttc tac aag aag ttt ata gaa gag 336
Ser Glu Gln Glu Gly Leu Glu Glu Phe Tyr Lys Lys Phe Ile Glu Glu
                100                105                110

agg att aaa gga gtg aaa gtt ggg aat aaa tgc acg att atg atg tat 384
Arg Ile Lys Gly Val Lys Val Gly Asn Lys Cys Thr Ile Met Met Tyr
                115                120                125

gga cct act ggt gct gga aag agt cat act atg ttt ggt tgt ggg aaa 432
Gly Pro Thr Gly Ala Gly Lys Ser His Thr Met Phe Gly Cys Gly Lys
    130                135                140

gag cct ggg att gtg tat cgt tct ttg aga gat ata ttg gga gat tct 480
Glu Pro Gly Ile Val Tyr Arg Ser Leu Arg Asp Ile Leu Gly Asp Ser
    145                150                155                160

gat caa gat ggt gtt act ttt gtt caa gtt act gtt ctt gag gtt tat 528
Asp Gln Asp Gly Val Thr Phe Val Gln Val Thr Val Leu Glu Val Tyr
                165                170                175

aat gag gag att tat gat ctt ctt tcg act aat agt agt aac aat tta 576
Asn Glu Glu Ile Tyr Asp Leu Leu Ser Thr Asn Ser Ser Asn Asn Leu
                180                185                190

ggt att ggt tgg cct aaa gga gca agc act aag gtaaaagtttc ttgattgata 629
Gly Ile Trp Pro Lys Gly Ala Ser Thr Lys
    195                200

acttttagtat acattgaatt ggctttaaaag gtgtgtactt tgttgttttg ttacag gtg 688
Val

agg ctt gaa gta atg ggg aaa aag gcg aaa aac gca agt ttt att tct 736
Arg Leu Glu Val Met Gly Lys Lys Ala Lys Asn Ala Ser Phe Ile Ser
    205                210                215                220

ggg aca gag gct ggg aag att tct aaa gaa att gtc aaa gtg gag aaa 784
Gly Thr Glu Ala Gly Lys Ile Ser Lys Glu Ile Val Lys Val Glu Lys
                225                230                235

cgg aga att gtg aag agt aca ctt tgt aac gaa aga agt tct cgg agt 832
Arg Arg Ile Val Lys Ser Thr Leu Cys Asn Glu Arg Ser Ser Arg Ser
                240                245                250

cac tgc att gtaagaacga tcttcttgat tgatgtgtat gcatagcttt 881

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His Cys Ile  
255

atgcagctta tctctgtttt aacttactag tgtggttggt tctttttgta g atc ata 938  
Ile Ile

ctt gat gtg cca act gtt ggg gga aga ttg atg ctt gtt gac atg gct 986  
Leu Asp Val Pro Thr Val Gly Gly Arg Leu Met Leu Val Asp Met Ala  
260 265 270

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275 280 285

atg caa gtaatgtttc ctctctcaat ttgtttgatt ctactaaagt tattgtagtt 1090  
Met Gln  
290

atggatatca actgacttat atctctcatt attcaacag act gct aag atc aac 1144  
Thr Ala Lys Ile Asn  
295

cag gga aat att gca ctg aag cga gtt gtg gaa tct ata gca aat gga 1192  
Gln Gly Asn Ile Ala Leu Lys Arg Val Val Glu Ser Ile Ala Asn Gly  
300 305 310

gat tct cat gta ccc ttt aga gac agc aag ctg acc atg ctt ctc cag 1240  
Asp Ser His Val Pro Phe Arg Asp Ser Lys Leu Thr Met Leu Leu Gln  
315 320 325

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Asp Ser Phe Glu Asp  
330

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335 340 345

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Glu Met His Lys Thr Leu Cys Thr Leu Glu Tyr Gly Ala Lys Ala Lys  
350 355 360 365

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Cys Ile Val Arg Gly Ser His Thr Pro Asn Lys Asp Lys Tyr Gly Gly  
370 375 380

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Asp Glu Ser Ala Ser Ala Val Ile Leu Gly Ser Arg Ile Ala Ala Met  
385 390 395

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400 405 410

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Glu Arg Asn Glu Ala Gln Lys Gln Leu Lys Lys Lys Glu Glu Glu Val	
415 420 425	
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430 435 440 445	
gaa gag gag ata aaa gag aaa gta aac gag aga acc cag ctt ttg aag	1739
Glu Glu Glu Ile Lys Glu Lys Val Asn Glu Arg Thr Gln Leu Leu Lys	
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Phe Val Glu Met Glu Arg Arg Met Glu Glu Arg Ile Val Gln Gln	
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Gln Glu Glu Leu Glu Met Met Arg Arg Arg Leu Glu Glu Ile Glu Val	
495 500 505	
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Glu Phe Arg Arg Ser Asn Gly Gly Ser Val Asp Glu Thr Ser Gly Phe	
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Ala Lys Arg Leu Arg Ser Leu Tyr Ser Asp Asp Asp Pro Gly Met Val	
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Lys Ser Met Asp Leu Asp Met Gly Asp Pro Glu Pro Val Lys Gln Val	
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610 615 620	
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Ile Thr Thr Pro Met Pro Ser Leu Asn Ser Glu Gly Leu Gly Lys Glu	
625 630 635	
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Asn Cys Phe Asn Gly Ala Asp Asp Lys Glu Ser Ala Ser Ser Arg Arg	

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ctt caa cct gca agc cca ctt cca ctt aat ccc ata gaa aac atg atg Leu Gln Pro Ala Ser Pro Leu Pro Leu Asn Pro Ile Glu Asn Met Met 835 840 845			2945
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885                      890

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la Asp Glu Pro Gly Leu Val  
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 Ser Glu Asn Ile Glu Phe Asn Gly Glu Asp Ser Ala Ile Gly Val Thr  
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 Val Ile Gly Glu Val Glu Glu Ala Glu Met Leu Arg  
                                   500                                  505

<210> 43  
 <211> 729  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
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 <222> (26)..(718)

<400> 43  
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                                   Met Phe Ala Asn Lys Phe Pro Gly Val  
   1                                  5  
 tac gca gcc act tgt ctc tcc gtc gaa gac gcc gtc aac gct cga tca 100  
 Tyr Ala Ala Thr Cys Leu Ser Val Glu Asp Ala Val Asn Ala Arg Ser  
   10                                  15                                  20                                  25  
 ata agc aat tgc aat gtc ctc gca ttc tcc ggc atc aaa aca tcc ccg 148  
 Ile Ser Asn Cys Asn Val Leu Ala Phe Ser Gly Ile Lys Thr Ser Pro  
                                   30                                  35                                  40  
 gaa acc gcc ttg gaa atc ttc gac gct tgg atc aaa act cct ttc aaa 196  
 Glu Thr Ala Leu Glu Ile Phe Asp Ala Trp Ile Lys Thr Pro Phe Lys  
                                   45                                  50                                  55  
 tct cct tgt cct gcg tcc gga tcc gaa cca tgg agc tca gtt atc tct 244  
 Ser Pro Cys Pro Ala Ser Gly Ser Glu Pro Trp Ser Ser Val Ile Ser  
                                   60                                  65                                  70  
 tcc ttc ctc gac aat tct ctc tcc gag atg tct cag att gga aag tca 292  
 Ser Phe Leu Asp Asn Ser Leu Ser Glu Met Ser Gln Ile Gly Lys Ser  
                                   75                                  80                                  85  
 acc gcc ggc gat tca aca acc aag aag atc gat gaa aca acc gcg tct 340  
 Thr Ala Gly Asp Ser Thr Thr Lys Lys Ile Asp Glu Thr Thr Ala Ser  
   90                                  95                                  100                                  105  
 tgc gta att tgc tgc ttg gcg aag aac aga gag ttc act cca gtg gac 388

Cys Val Ile Cys Cys Leu Ala Lys Asn Arg Glu Phe Thr Pro Val Asp  
 110 115 120  
 atc atg ccg gga ggc tcg atg aag atc gtt aga gag acg ccg acg tcg 436  
 Ile Met Pro Gly Gly Ser Met Lys Ile Val Arg Glu Thr Pro Thr Ser  
 125 130 135  
 gcg att gta aga ttc aaa gcg gga agt gtg gaa ccg gcg cat cac cac 484  
 Ala Ile Val Arg Phe Lys Ala Gly Ser Val Glu Pro Ala His His His  
 140 145 150  
 aca ttc ggc cat gac ctt gta gtc ata aag gga aag aaa agt gtg tgg 532  
 Thr Phe Gly His Asp Leu Val Val Ile Lys Gly Lys Lys Ser Val Trp  
 155 160 165  
 aat ctg agc aag aag gag aga gct gat ctc gtt gac ggc gat tac cta 580  
 Asn Leu Ser Lys Lys Glu Arg Ala Asp Leu Val Asp Gly Asp Tyr Leu  
 170 175 180 185  
 ttc act ccc gcc ggt gat gtt cac cga gtc aaa tat cac gaa gac act 628  
 Phe Thr Pro Ala Gly Asp Val His Arg Val Lys Tyr His Glu Asp Thr  
 190 195 200  
 gag ttc ttc atc act tgg gat ggc cat tgg gac ata ttc ctt gac gaa 676  
 Glu Phe Phe Ile Thr Trp Asp Gly His Trp Asp Ile Phe Leu Asp Glu  
 205 210 215  
 gac ctc gaa act gca aag aaa gcc atc gaa gaa gaa gct tga 718  
 Asp Leu Glu Thr Ala Lys Lys Ala Ile Glu Glu Glu Ala  
 220 225 230  
 aggtgtaaac t 729

<210> 44  
 <211> 230  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 44  
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 1 5 10 15  
 Val Glu Asp Ala Val Asn Ala Arg Ser Ile Ser Asn Cys Asn Val Leu  
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 Ala Phe Ser Gly Ile Lys Thr Ser Pro Glu Thr Ala Leu Glu Ile Phe  
 35 40 45  
 Asp Ala Trp Ile Lys Thr Pro Phe Lys Ser Pro Cys Pro Ala Ser Gly  
 50 55 60  
 Ser Glu Pro Trp Ser Ser Val Ile Ser Ser Phe Leu Asp Asn Ser Leu  
 65 70 75 80  
 Ser Glu Met Ser Gln Ile Gly Lys Ser Thr Ala Gly Asp Ser Thr Thr  
 85 90 95

Lys Lys Ile Asp Glu Thr Thr Ala Ser Cys Val Ile Cys Cys Leu Ala  
 100 105 110  
 Lys Asn Arg Glu Phe Thr Pro Val Asp Ile Met Pro Gly Gly Ser Met  
 115 120 125  
 Lys Ile Val Arg Glu Thr Pro Thr Ser Ala Ile Val Arg Phe Lys Ala  
 130 135 140  
 Gly Ser Val Glu Pro Ala His His His Thr Phe Gly His Asp Leu Val  
 145 150 155 160  
 Val Ile Lys Gly Lys Lys Ser Val Trp Asn Leu Ser Lys Lys Glu Arg  
 165 170 175  
 Ala Asp Leu Val Asp Gly Asp Tyr Leu Phe Thr Pro Ala Gly Asp Val  
 180 185 190  
 His Arg Val Lys Tyr His Glu Asp Thr Glu Phe Phe Ile Thr Trp Asp  
 195 200 205  
 Gly His Trp Asp Ile Phe Leu Asp Glu Asp Leu Glu Thr Ala Lys Lys  
 210 215 220  
 Ala Ile Glu Glu Glu Ala  
 225 230

<210> 45  
 <211> 1203  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (12)..(1193)

<400> 45  
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 Met Thr Ile Arg Asn Gln Arg Phe Ser Leu Leu Lys Gln  
 1 5 10  
 cct ata tcc tcc aca ctt aat cag cat tta gta gat tat cca acc ccg 98  
 Pro Ile Ser Ser Thr Leu Asn Gln His Leu Val Asp Tyr Pro Thr Pro  
 15 20 25  
 agc aat ctt agt tat tgg tgg ggg ttc ggt ccg tta gct ggt att tgt 146  
 Ser Asn Leu Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys  
 30 35 40 45  
 tta gtc att cag ata gtg act ggc gtt ttt tta gct atg cat tac aca 194  
 Leu Val Ile Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr  
 50 55 60  
 cct cat gtg gat tta gct ttc aac agc gta gaa cac att atg aga gat 242

Pro His Val Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp	
65 70 75	
ggt gaa ggg ggc tgg ttg ctc cgt tat atg cat gct aat ggg gca agt	290
Val Glu Gly Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser	
80 85 90	
atg ttt ctt att gtg gtt tac ctt cat att ttt cgt ggt cta tat cat	338
Met Phe Leu Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His	
95 100 105	
gcg agt tat agc agt cct agg gaa ttt gtt tgg tgt ctt gga gtt gta	386
Ala Ser Tyr Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val	
110 115 120 125	
atc ttc cta tta atg att gtg aca gct ttt ata gga tat gta cta cct	434
Ile Phe Leu Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro	
130 135 140	
tgg ggt cag atg agc ttt tgg gga gct aca gta att aca agc tta gct	482
Trp Gly Gln Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala	
145 150 155	
agc gcc ata cct gta gta gga gat acc ata gtg act tgg ctt tgg ggt	530
Ser Ala Ile Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly	
160 165 170	
ggt ttc tcc gtg gac aat gcc acc tta aat cgt ttt ttt agt ctt cat	578
Gly Phe Ser Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His	
175 180 185	
cat tta ctc ccc ttt att tta gta ggc gcc agt ctt ctt cat ctg gcc	626
His Leu Leu Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala	
190 195 200 205	
gca ttg cat caa tat gga tca aat aat cca ttg ggt gta cat tct gag	674
Ala Leu His Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu	
210 215 220	
atg gat aaa ata gct ttt tac cct tat ttt tat gtc aag gat cta gtt	722
Met Asp Lys Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val	
225 230 235	
ggt tgg gta gct ttt gct atc ttt ttt tct att tgg att ttt tat gct	770
Gly Trp Val Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala	
240 245 250	
cct aat gtt ttg gga cat ccc gac aat tat ata cct gct aat ccg atg	818
Pro Asn Val Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met	
255 260 265	
tcc acc ccg cct cat att gtg ccg gaa tgg tat ttc cta ccg atc cat	866
Ser Thr Pro Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His	
270 275 280 285	
gcc att ctt cgt agt ata cct gac aaa gcg gga ggt gta gcc gca ata	914
Ala Ile Leu Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile	

290	295	300	
gca cca gtt ttt ata tgt ctc ttg gct tta cct ttt ttt aaa agt atg			962
Ala Pro Val Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met			
305	310	315	
tat gtg cgt agt tca agt ttt cga ccg att cac caa gga atg ttt tgg			1010
Tyr Val Arg Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp			
320	325	330	
ttg ctt ttg gcg gat tgc tta cta cta ggt tgg atc gga tgt caa cct			1058
Leu Leu Leu Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro			
335	340	345	
gtg gag gct cca ttt gtt act att gga caa att tct cct ttg gtt ttc			1106
Val Glu Ala Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe			
350	355	360	365
ttc ttg ttc ttt gcc ata acg ccc att ctg gga cga gtt gga aga gga			1154
Phe Leu Phe Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly			
370	375	380	
att cct aat tct tac acg gat gag act gat cac acc tga tcagtgaaaa			1203
Ile Pro Asn Ser Tyr Thr Asp Glu Thr Asp His Thr			
385	390		

&lt;210&gt; 46

&lt;211&gt; 393

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 46

Met Thr Ile Arg Asn Gln Arg Phe Ser Leu Leu Lys Gln Pro Ile Ser	
1 5 10 15	
Ser Thr Leu Asn Gln His Leu Val Asp Tyr Pro Thr Pro Ser Asn Leu	
20 25 30	
Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys Leu Val Ile	
35 40 45	
Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr Pro His Val	
50 55 60	
Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp Val Glu Gly	
65 70 75 80	
Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser Met Phe Leu	
85 90 95	
Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His Ala Ser Tyr	
100 105 110	
Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val Ile Phe Leu	
115 120 125	

Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro Trp Gly Gln  
 130 135 140  
 Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala Ser Ala Ile  
 145 150 155 160  
 Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly Gly Phe Ser  
 165 170 175  
 Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His His Leu Leu  
 180 185 190  
 Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala Ala Leu His  
 195 200 205  
 Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu Met Asp Lys  
 210 215 220  
 Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val Gly Trp Val  
 225 230 235 240  
 Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala Pro Asn Val  
 245 250 255  
 Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met Ser Thr Pro  
 260 265 270  
 Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His Ala Ile Leu  
 275 280 285  
 Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile Ala Pro Val  
 290 295 300  
 Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met Tyr Val Arg  
 305 310 315 320  
 Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp Leu Leu Leu  
 325 330 335  
 Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro Val Glu Ala  
 340 345 350  
 Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe Phe Leu Phe  
 355 360 365  
 Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly Ile Pro Asn  
 370 375 380  
 Ser Tyr Thr Asp Glu Thr Asp His Thr  
 385 390

&lt;210&gt; 47

&lt;211&gt; 1194

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1194)

&lt;400&gt; 47

atg aga aaa gtt tct tcc gta att tct gtc gtt gat ccc gtt att ttc	48
Met Arg Lys Val Ser Ser Val Ile Ser Val Val Asp Pro Val Ile Phe	
1 5 10 15	
cga gga aat tac gca gct aca ctc gat gtg tcg tat ccg gta ttc ccg	96
Arg Gly Asn Tyr Ala Ala Thr Leu Asp Val Ser Tyr Pro Val Phe Pro	
20 25 30	
caa aat aaa gat ggc cgt gca ctt cag aaa gtt ctc gga acc att cgt	144
Gln Asn Lys Asp Gly Arg Ala Leu Gln Lys Val Leu Gly Thr Ile Arg	
35 40 45	
aac gga gat ttg gct gtt tcg gct cct aaa aca agt ctt agg gca ggt	192
Asn Gly Asp Leu Ala Val Ser Ala Pro Lys Thr Ser Leu Arg Ala Gly	
50 55 60	
att ttc ggt gaa ggt tcc agc ttg gtc gat cag atg ccc tgt aaa gtt	240
Ile Phe Gly Glu Gly Ser Ser Leu Val Asp Gln Met Pro Cys Lys Val	
65 70 75 80	
tac gtg gcg ttc cac aaa gaa tca tac tgc tcg ctt acc ggg cta agc	288
Tyr Val Ala Phe His Lys Glu Ser Tyr Cys Ser Leu Thr Gly Leu Ser	
85 90 95	
aaa cgc gga gtc gca ata aac gaa gca agt ctt tcc ctg gtc gga atc	336
Lys Arg Gly Val Ala Ile Asn Glu Ala Ser Leu Ser Leu Val Gly Ile	
100 105 110	
act aaa gtt aga gcc ccc gtc gga aat acc gtt gga gcg gaa gca acc	384
Thr Lys Val Arg Ala Pro Val Gly Asn Thr Val Gly Ala Glu Ala Thr	
115 120 125	
gta tac ata ggt agt cca aaa cct tat aca gag tgt agt act cca aat	432
Val Tyr Ile Gly Ser Pro Lys Pro Tyr Thr Glu Cys Ser Thr Pro Asn	
130 135 140	
aaa atg tat gcg gtt gca gct ggt ttc aag gtg gca agt ttc gcc gct	480
Lys Met Tyr Ala Val Ala Ala Gly Phe Lys Val Ala Ser Phe Ala Ala	
145 150 155 160	
agt acg tgc gta cgt ccg cct gca cgt gca cgt cgt acg ctg acc gtg	528
Ser Thr Cys Val Arg Pro Pro Ala Arg Ala Arg Arg Thr Leu Thr Val	
165 170 175	
acg tcg acc gtg acg ctg tct atg gca act ggt aaa tgc gta aat aca	576
Thr Ser Thr Val Thr Leu Ser Met Ala Thr Gly Lys Cys Val Asn Thr	
180 185 190	
gga aac gaa cca gta tct aaa cct aca gga gta cgt atg atg tta att	624
Gly Asn Glu Pro Val Ser Lys Pro Thr Gly Val Arg Met Met Leu Ile	
195 200 205	

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cct ctc gat gct act ctc att aaa gta tgg act ggg gaa gta aaa aaa 672
Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys
210 215 220

gcg ata gtt tcc cgg cct gca aaa att ttc aat agc gta gga aat tta 720
Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu
225 230 235 240

gaa cgt cct tca att tcg cat tct tgt gga caa ggt ttg gat gaa gct 768
Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala
245 250 255

gcc gct tat atc aag ggt aga ctt tct cca atc gtt aaa gca gaa aga 816
Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg
260 265 270

att aaa gtt ttg gtt aaa gac gag cac gaa gaa gta aaa gaa ctt ctt 864
Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu
275 280 285

caa gaa ggt tac gaa gaa atc gtc ggt gag tct cca agt ttc aat tta 912
Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu
290 295 300

gca caa gaa gcg tgg gaa aaa gct gaa aga cga gca aaa ggt cag tcc 960
Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser
305 310 315 320

ccg tgc agt gcg gca aaa gca aac ctt gca acc tac tat ttt tca aca 1008
Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
325 330 335

ggg gat ttc gaa aaa tca att aaa ctc tac gaa gaa cct atg ggt ttg 1056
Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
340 345 350

aaa gat act gat aag agc tat ctg cga gaa cgt aga aaa aga gta gag 1104
Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
355 360 365

gct act acg ttg cgt gca ccg ttc gtg gtc cag ctg acc gtg cgt agt 1152
Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser
370 375 380

cgt acg acg atg atc gcc gtt ggt gaa agc aac gca aac tga 1194
Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn
385 390 395

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&lt;210&gt; 48

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 48

Met Arg Lys Val Ser Ser Val Ile Ser Val Val Asp Pro Val Ile Phe

1	5	10	15
Arg Gly Asn Tyr Ala Ala Thr Leu Asp Val Ser Tyr Pro Val Phe Pro	20	25	30
Gln Asn Lys Asp Gly Arg Ala Leu Gln Lys Val Leu Gly Thr Ile Arg	35	40	45
Asn Gly Asp Leu Ala Val Ser Ala Pro Lys Thr Ser Leu Arg Ala Gly	50	55	60
Ile Phe Gly Glu Gly Ser Ser Leu Val Asp Gln Met Pro Cys Lys Val	65	70	75
Tyr Val Ala Phe His Lys Glu Ser Tyr Cys Ser Leu Thr Gly Leu Ser	85	90	95
Lys Arg Gly Val Ala Ile Asn Glu Ala Ser Leu Ser Leu Val Gly Ile	100	105	110
Thr Lys Val Arg Ala Pro Val Gly Asn Thr Val Gly Ala Glu Ala Thr	115	120	125
Val Tyr Ile Gly Ser Pro Lys Pro Tyr Thr Glu Cys Ser Thr Pro Asn	130	135	140
Lys Met Tyr Ala Val Ala Ala Gly Phe Lys Val Ala Ser Phe Ala Ala	145	150	155
Ser Thr Cys Val Arg Pro Pro Ala Arg Ala Arg Arg Thr Leu Thr Val	165	170	175
Thr Ser Thr Val Thr Leu Ser Met Ala Thr Gly Lys Cys Val Asn Thr	180	185	190
Gly Asn Glu Pro Val Ser Lys Pro Thr Gly Val Arg Met Met Leu Ile	195	200	205
Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys	210	215	220
Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu	225	230	235
Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala	245	250	255
Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg	260	265	270
Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu	275	280	285
Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu	290	295	300
Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser			

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305              310              315              320
Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
              325              330              335
Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
              340              345              350
Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
              355              360              365
Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser
              370              375              380
Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn
385              390              395

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<210> 49
<211> 611
<212> DNA
<213> Arabidopsis thaliana

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<220>
<221> CDS
<222> (5)..(601)

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      Met Ile Val Leu Ser Val Gly Ser Ala Ser Ser Ser Pro Ile Val
        1              5              10              15

gtc gtc ttt tcc gtc gcg ctt ctt ctg ttc tac ttc tct gaa act tct 97
Val Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser
              20              25              30

cta gga gct cct tgt ccc atc aat ggc ttg cca atc gtg agg aat att 145
Leu Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile
              35              40              45

agt gac ctt cct cag gat aac tat gga aga cca ggt ctt tcc cac atg 193
Ser Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met
              50              55              60

act gtt gct ggc tcc gta ttg cat gga atg aaa gag gtt gaa ata tgg 241
Thr Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp
              65              70              75

ctt cag aca ttt gct cca ggt tca gag aca cca att cac agg cac tcc 289
Leu Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser
              80              85              90              95

tgt gaa gag gtt ttt gtt gtc cta aag ggc agt ggt act ctg tat ctc 337
Cys Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu
              100              105              110

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gct gaa aca cat gga aat ttc cct ggg aaa cca atc gaa ttt cca atc 385
Ala Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile
      115                      120                      125

ttt gcc aac agt aca att cat att ccg atc aat gat gct cat cag gtc 433
Phe Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val
      130                      135                      140

aaa aac acc ggt cat gag gac ctg cag gtg ttg gtt atc ata tct cgg 481
Lys Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg
      145                      150                      155

ccg cct att aaa atc ttc atc tac gaa gac tgg ttt atg cca cac act 529
Pro Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr
      160                      165                      170                      175

gct gca agg ctg aag ttc cct tac tat tgg gat gag caa tgc att caa 577
Ala Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln
      180                      185                      190

gaa tca caa aaa gac gag ctt taa agcaaagtcc 611
Glu Ser Gln Lys Asp Glu Leu
      195

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<210> 50
<211> 198
<212> PRT
<213> Arabidopsis thaliana

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<400> 50
Met Ile Val Leu Ser Val Gly Ser Ala Ser Ser Ser Pro Ile Val Val
  1                      5                      10                      15

Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser Leu
      20                      25                      30

Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile Ser
      35                      40                      45

Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met Thr
      50                      55                      60

Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp Leu
      65                      70                      75                      80

Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser Cys
      85                      90                      95

Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu Ala
      100                      105                      110

Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile Phe
      115                      120                      125

Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val Lys
      130                      135                      140

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Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg Pro  
 145 150 155 160

Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr Ala  
 165 170 175

Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln Glu  
 180 185 190

Ser Gln Lys Asp Glu Leu  
 195

<210> 51  
 <211> 1398  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (1)..(1398)

<400> 51  
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 Met Pro Arg Arg Arg Thr Cys Cys Arg Arg Glu Phe Gly Pro Thr Gln  
 1 5 10 15

cca tgt aga ggc gcg tca atc act gga tct cta cgt gac cgt cga ccg 96  
 Pro Cys Arg Gly Ala Ser Ile Thr Gly Ser Leu Arg Asp Arg Arg Pro  
 20 25 30

acc gct atc ctt atc gga acc ctc acc gct tta ggc ggt gga gtt aga 144  
 Thr Ala Ile Leu Ile Gly Thr Leu Thr Ala Leu Gly Gly Gly Val Arg  
 35 40 45

tgt ggc tct tgc ccc agt gtc gac cgt tgc gga cac gca agt gcc gcc 192  
 Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala  
 50 55 60

ata gcg cgt gat agc tgt gcc gtg ttc gca tgg aag cga ggt acg cga 240  
 Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg  
 65 70 75 80

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 Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly  
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ggg gga ccc gac ttc gat tgt gat gat ggt ggt gac gat ccg ctt ttg 336  
 Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu  
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att caa gat ggc gta aaa gct gcg gag gaa tat gct aaa tct gga aaa 384  
 Ile Gln Asp Gly Val Lys Ala Ala Glu Glu Tyr Ala Lys Ser Gly Lys  
 115 120 125

gtt cca gat cca agc tgt act gat aat gct gag ttt caa gtt gtg ctt	432
Val Pro Asp Pro Ser Cys Thr Asp Asn Ala Glu Phe Gln Val Val Leu	
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Arg Pro Ser Cys Leu Val Gly Val Ser Glu Glu Thr Thr Thr Gly Val	
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Lys Arg Ser Tyr Gln Met Gln Pro Lys Cys Thr Leu Leu Leu His Ala	
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act gat gtt tgt gac acc gtg atc aag agc aag att gat aac ttg tac	624
Thr Asp Val Cys Asp Thr Val Ile Lys Ser Lys Ile Asp Asn Leu Tyr	
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Gly Cys Arg His Ser Leu Ser Asp Gly Leu Met Arg Ala Thr Asp Val	
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Arg Arg Pro Cys Lys Val Ala Leu Val Gly Gly Tyr Gly Asp Val Phe	
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Lys Gly Trp Val Ala Ala Leu Lys Gln Ala Gly Ala Arg Val Ile Val	
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Thr Glu Ile Pro Gln Ile Cys Ala Val Gln Ala Thr Met Glu Gly Ser	
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Ser Val Leu Thr Leu Glu Asp Val Val Ser Asp Val Asp Arg Phe Val	
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Thr Thr Thr Gly Asn Lys Asp Leu Ile Met Val Asp His Met Arg Arg	
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atc gac atg cgc agt ctc gag acc ttc cct gga gtg aag cgg atc aca	1008
Ile Asp Met Arg Ser Leu Glu Thr Phe Pro Gly Val Lys Arg Ile Thr	
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Ile Lys Ala Gln Thr Asp Arg Trp Val Phe Arg Asp Thr Asn Arg Gly	
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 385 390 395 400

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cat ctc gta aag ctc gga gca agg ctc act aag ctt agt cgg tgc acg 1296  
 His Leu Val Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr  
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Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala  
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Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu

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Ser	Val	Leu	Thr	Leu	Glu	Asp	Val	Val	Ser	Asp	Val	Asp	Arg	Phe	Val		
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Ser	Gln	Leu	Glu	Leu	Trp	Arg	Glu	Lys	Ser	Thr	Gly	Lys	Tyr	Glu	Lys		
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Asp Val Asp Glu Ile Val Arg Leu Arg Lys Arg Phe Phe Lys Leu Asp						96
	20		25		30	
 aga gat tgt tca gga tca gaa ctt gga agt gag ttc atg agt ttg cct						
Arg Asp Cys Ser Gly Ser Glu Leu Gly Ser Glu Phe Met Ser Leu Pro						144
	35		40		45	
 caa gtt agt tcg aac cct ctt cgg atg cgt gag atg cgt aat ttc gat						
Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp						192
	50		55		60	
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Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg						240
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Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala						288
	85		90		95	
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Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu						336
	100		105		110	
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Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn						384
	115		120		125	
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Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp						432

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 Asp Val  
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 35 40 45  
 Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp  
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 Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg  
 65 70 75 80  
 Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala  
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 Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu  
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 Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp  
 130 135 140  
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 Trp Ala Val Asn Pro Cys Phe Ile Ala Ser Cys Ser Cys Leu Leu Val  
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ggc ttc ggc gac gca atc ttc tac gag tcg ttc gcc ggg gat ttt gat 147  
 Gly Phe Gly Asp Ala Ile Phe Tyr Glu Ser Phe Ala Gly Asp Phe Asp  
 35 40 45

gca cgc tgg att tta tcc ggc tca aag tgt ctc tcg gat tcg gcc aag 195  
 Ala Arg Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys  
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aat gct ggg ttt gat gat tat gga ctt ctt gtg ggt gaa caa gcc agg 243  
 Asn Ala Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg  
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aag cct cct ata gtc aag gaa ctt gcc gag tct ctc agt cta aag gac 291  
 Lys Pro Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp  
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gga aga gtt gtt ctt gag tgt gag act cgc ctt gac cat ggc atc gac 339  
 Gly Arg Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp  
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 Cys Gly Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp  
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 Arg Thr Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu  
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Cys Val Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys	
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Val Pro Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln	
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Ile Leu Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys	
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Glu Asp Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn	
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Pro Ser Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly	
225 230 235	
cca agt gcc ctg aag cga cag gaa agc gat gag gat ccg aac cgg gaa	771
Pro Ser Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu	
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Ile Leu His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His	
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Ala Lys Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu	
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Lys Asp Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly	
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Ala Ala Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro	
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aat tat aag gga aaa ccc tcc gtg ggt cca aac gtt tac caa ggg att	1011
Asn Tyr Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile	
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Trp Lys Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys	
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Pro Ala Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln	
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 Glu Tyr Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His  
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 415 420 425 430  
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 480 485 490  
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 Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys Asn Ala  
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Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg Lys Pro  
 65 70 75 80  
 Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp Gly Arg  
 85 90 95  
 Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp Cys Gly  
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 Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp Lys Phe  
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 Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg Arg Thr  
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 260 265 270  
 Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu Lys Asp  
 275 280 285  
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 Gly Ser Ser Pro Met Arg Trp Ala Trp Lys Arg Trp Gln Ala Val Gly  
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 Ala Ser Thr Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile  
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Thr	Thr	Ser	Thr	Arg	Ala	Arg	Arg	Tyr	Ala	Val	Ser	Ala	Lys	Phe	Pro	
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aga	tta	agt	aat	aag	ggc	aaa	gat	tac	atg	cgt	tgc	gtc	ctc	caa	tac	291
Arg	Leu	Ser	Asn	Lys	Gly	Lys	Asp	Tyr	Met	Arg	Cys	Val	Leu	Gln	Tyr	
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Thr	Val	Lys	Asn	Glu	Gln	Lys	Val	Asp	Cys	Gly	Gly	Ser	Tyr	Ile	Lys	
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Leu	Leu	Pro	Ser	Lys	Leu	Arg	Thr	Gly	Asp	Gly	Asp	Gly	Val	Ser	Glu	
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Tyr	Ser	Ile	Met	Phe	Gly	Pro	Asp	Ser	Thr	Gly	Ala	Ser	Arg	Thr	Val	
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Gln	Asn	Lys	Val	Glu	Thr	Asp	Gln	Leu	Thr	His	Gln	Tyr	Thr	Thr	Ser	
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Trp	Ser	Pro	Asp	Trp	Thr	Tyr	Asn	Val	Leu	Val	Asp	Asn	Lys	Glu	Ser	
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Gln	Ala	Gly	Asn	Leu	Ala	Asp	Asp	Cys	Glu	Leu	Leu	Pro	Gln	Lys	Arg	
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Asp	Val	Lys	His	His	Ala	Pro	Arg	Arg	Asn	Val	Lys	Pro	Ala	Gly	His	
		225					230					235				
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Asp	Asp	Ile	Pro	Ala	Arg	Arg	Thr	Thr	Pro	Glu	Ala	Val	Arg	Lys	Gly	
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Arg	Thr	Asn	Glu	Arg	Pro	Asp	Arg	Thr	Trp	Ala	Thr	Gly	Thr	Thr	Pro	
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 Gly Thr Arg Thr Trp Thr Val Lys Ser Gly Ser Ile Thr Asn Asn Met  
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 Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro Arg Leu Ser  
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Ser	Lys	Leu	Arg	Thr	Gly	Asp	Gly	Asp	Gly	Val	Ser	Glu	Tyr	Ser	Ile	
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Thr	Ser	Val	Glu	Thr	Ala	Thr	Asp	Phe	Ser	Glu	Lys	Thr	Lys	Val	Ala	
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Gly	Ala	Glu	Arg	His	Cys	Ala	Asp	Glu	Arg	Trp	Lys	Glu	Thr	Thr	Val	
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Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr  
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gag gct gag ctc caa gac atg atc aac gag gtt gat gca gat gga aac 144  
Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn  
35 40 45

ggc act atc gac ttc ccc gag ttc ctg aac ctg atg gct aag aag atg 192  
Gly Thr Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Lys Lys Met  
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Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met  
100 105 110

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 Gly Thr Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Lys Lys Met  
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 Lys Asp Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe  
   65                  70                  75                  80  
 Asp Lys Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val  
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 Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met  
           100                  105                  110  
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Asp Ser Ser Asp Arg Ser Thr Pro Pro Ser Leu Asp Glu Arg Ile Asp
      160                      165                      170

ctc gtt gga aag ctc ttc aaa aaa act ttg aag cgt gtt gaa ctc agg 757
Leu Val Gly Lys Leu Phe Lys Lys Thr Leu Lys Arg Val Glu Leu Arg
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gac gaa ctt ttt gcc caa atc tcc aaa cag act aga cat aat cct gac 805
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Arg Gln Tyr Leu Ile Lys Ala Trp Glu Leu Met Tyr Leu Cys Ala Ser
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Ser Met Pro Pro Ser Lys Asp Ile Gly Gly Tyr Leu Ser Glu Tyr Ile
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His Asn Val Ala His Asp Ala Thr Ile Glu Pro Asp Ala Gln Val Leu
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      890

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His Ala Trp Lys Asp Asp Lys Arg Lys Gln His Ile Tyr Asp Arg Val
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580 585 590	
atg gaa cca tca aca gtt tcg aag gaa ttt agg tcg atc att tct gaa	1824
Met Glu Pro Ser Thr Val Ser Lys Glu Phe Arg Ser Ile Ile Ser Glu	
595 600 605	
tgt tta cga aac gat gca act gaa aga caa aca gct tca aac tta gta	1872
Cys Leu Arg Asn Asp Ala Thr Glu Arg Gln Thr Ala Ser Asn Leu Val	

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Asn His Glu Phe Val Lys Lys Tyr Gln Lys Tyr Asn Arg Glu Lys Trp
625                630                635                640

acc gca gat tta caa agg tgg caa taa aaatcgctt cagcctgat 1967
Thr Ala Asp Leu Gln Arg Trp Gln
645

cgctgacgct cgacgcctgc ccccgctgc cagctcgccc agctcgccca ggctcgccca 2027
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Asn Asn Asn Pro Lys Ser His Asn Ser His Asn Ser Asn Gly Met Thr
                35                40                45
Gly Asn Arg Asn Asn Asn Asn Lys Asn Ala Gly Gly Val Glu Thr Ser
                50                55                60
Lys Lys Ala Arg Ser Arg Leu Glu Thr His Pro Arg Asp Asn Glu Asn
                65                70                75                80
Asn Tyr Arg Leu Ala Thr Ser Ala Gly Thr Lys Gly Gly Ala Arg Thr
                85                90                95
Val Asp Val Pro Val Ile Leu Ser Thr Arg Glu Ser Gln Gly Thr Arg
                100                105                110
Ser Val Asn Ala Thr Ser Lys Ile Arg Cys Pro Asp Ser Thr Ala Ile
                115                120                125
Cys Glu Trp Phe Ala Thr Pro Thr Asp Pro Gln Arg Pro Gly Val Tyr
                130                135                140
Asn His Lys Asn Gly Asp Lys Asn Asn Arg Asp Thr Gly Asn Ile Asn
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Thr Val Ser Ser Leu Met Asp Asn Ala Arg Gly Pro Asn Pro Arg Ser
                165                170                175
Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr

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225						230					235				240
Ser	Pro	Ala	Ile	Asn	Ala	Val	Lys	Ser	Ala	Ser	Asn	Arg	Ser	Ser	Ala
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His	Tyr	Ala	Arg	Ser	Gly	Thr	Tyr	Gln	Ile	Asn	Ala	Val	Thr	Val	Leu
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Arg	Val	Leu	Gly	Arg	Gly	Ala	Arg	Arg	Asp	Val	Lys	Ser	Ala	Tyr	His
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Gln	Glu	Asn	Ile	Arg	Asn	Arg	Ile	Ile	Leu	Glu	Leu	Arg	Thr	Leu	His
				325					330					335	
Lys	Thr	Ser	Tyr	Gln	Tyr	Ile	Val	Pro	Tyr	Tyr	Asp	Gly	Ile	Tyr	Thr
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Glu	Gly	Ser	Ile	Phe	Ile	Arg	Met	Val	Glu	Leu	Gly	Trp	Val	Thr	Asn
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Lys	Cys	Pro	Ser	Lys	Arg	Asp	Ile	Lys	Pro	Ser	Asp	Ile	Leu	Val	Asn
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Asn	Glu	Gly	Arg	Ala	Lys	Ile	Ala	Gly	Phe	Gly	Val	Ser	Gly	Gln	Leu
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Gln	His	Thr	Leu	Ser	Lys	Asp	Val	Thr	Ser	Val	Glu	Ser	Pro	Glu	Arg
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Arg	Ser	Gly	Arg	Ser	Tyr	Gly	Phe	Asp	Arg	Asp	Ile	Trp	Ser	Asp	Gly
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Ile	Thr	Arg	Val	Ser	Cys	Ala	Ile	Gly	Arg	Phe	Pro	Tyr	Ala	Cys	Asn
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Tyr	Pro	Gln	Gln	Leu	Pro	Gln	Ala	Ser	Gln	His	Gln	Leu	Gln	Gln	Gln

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Gln	Gln	Lys	Arg	Pro	Ala	Leu	Gln	Pro	Lys	Gln	Glu	Gln	Pro	Glu	Val				
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Glu	Lys	His	Arg	Leu	Gln	Ile	Pro	Arg	Gln	Asn	Leu	Ala	Val	Tyr	Asn				
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Ser	Asn	His	Asp	Ile	Trp	Asn	Asn	Arg	Asn	Arg	Asp	Lys	Tyr	Ile	Ile				
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Ser	Asn	Asn	Pro	Asn	Asn	Arg	Asn	Asp	Asn	Asn	Asn	Thr	Val	Cys	Asp				
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Leu	Ser	Ser	Gly	Glu	Leu	Gly	Glu	Ser	Arg	Glu	Val	Val	Pro	Asp	Gly				
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Ile	Gly	Leu	Glu	Val	Leu	Leu	Asp	Ser	Ile	Val	Lys	Glu	Glu	Val	Arg				
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Cys	Leu	Arg	Asn	Asp	Ala	Thr	Glu	Arg	Gln	Thr	Ala	Ser	Asn	Leu	Val				
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Asn	His	Glu	Phe	Val	Lys	Lys	Tyr	Gln	Lys	Tyr	Asn	Arg	Glu	Lys	Trp				
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cga ccg	tcg	gtt	ttc	tgt	tct	att	cca	ggt	ctc	ggc	ggc	gat	tcc	cac					100
Arg	Pro	Ser	Val	Phe	Cys	Ser	Ile	Pro	Gly	Leu	Gly	Gly	Asp	Ser	His				
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cga aaa	cct	cca	agt	gac	ggt	ttc	ctc	aag	ctg	cct	gcg	tcg	tct	att					148
Arg	Lys	Pro	Pro	Ser	Asp	Gly	Phe	Leu	Lys	Leu	Pro	Ala	Ser	Ser	Ile				
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ccg gcg	gac	agc	cga	aaa	tta	gta	gcg	aat	tct	act	tcc	ttt	cat	cca					196

Pro	Ala	Asp	Ser	Arg	Lys	Leu	Val	Ala	Asn	Ser	Thr	Ser	Phe	His	Pro	
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Ile	Ser	Ala	Val	Asn	Val	Ser	Ala	Gln	Ala	Ser	Leu	Thr	Ala	Asp	Phe	
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ccc	gcc	ctt	tca	gaa	act	ata	ctg	aaa	gag	gga	aga	aat	aac	gga	aaa	292
Pro	Ala	Leu	Ser	Glu	Thr	Ile	Leu	Lys	Glu	Gly	Arg	Asn	Asn	Gly	Lys	
		75				80				85						
gag	aaa	gca	gag	aac	atc	gtg	tgg	cac	gag	agt	tcg	ata	tgc	aga	tgc	340
Glu	Lys	Ala	Glu	Asn	Ile	Val	Trp	His	Glu	Ser	Ser	Ile	Cys	Arg	Cys	
	90				95					100					105	
gac	aga	caa	caa	ctt	ctt	caa	caa	aag	ggg	tgt	gtc	gtt	tgg	atc	act	388
Asp	Arg	Gln	Gln	Leu	Leu	Gln	Gln	Lys	Gly	Cys	Val	Val	Trp	Ile	Thr	
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ggg	ctc	agt	ggg	tca	ggg	aaa	agc	act	gtt	gct	tgt	gca	cta	agt	aaa	436
Gly	Leu	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Val	Ala	Cys	Ala	Leu	Ser	Lys	
			125				130						135			
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Ala	Leu	Phe	Glu	Arg	Gly	Lys	Leu	Thr	Tyr	Thr	Leu	Asp	Gly	Asp	Asn	
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Val	Arg	His	Gly	Leu	Asn	Arg	Asp	Leu	Thr	Phe	Lys	Ala	Glu	His	Arg	
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Thr	Glu	Asn	Ile	Arg	Arg	Ile	Gly	Glu	Val	Ala	Lys	Leu	Phe	Ala	Asp	
	170				175					180					185	
gtc	gga	gtc	att	tgt	ata	gca	agt	ttg	att	tct	ccg	tac	cgg	aga	gac	628
Val	Gly	Val	Ile	Cys	Ile	Ala	Ser	Leu	Ile	Ser	Pro	Tyr	Arg	Arg	Asp	
				190					195					200		
aga	gac	gcg	tgc	cgg	tcc	ttg	tta	cct	gac	ggc	gat	ttc	gtc	gag	gtc	676
Arg	Asp	Ala	Cys	Arg	Ser	Leu	Leu	Pro	Asp	Gly	Asp	Phe	Val	Glu	Val	
		205						210					215			
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Phe	Met	Asp	Val	Pro	Leu	His	Val	Cys	Glu	Ser	Arg	Asp	Pro	Lys	Gly	
		220					225					230				
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Leu	Tyr	Lys	Leu	Ala	Arg	Ala	Gly	Lys	Ile	Lys	Gly	Phe	Thr	Gly	Ile	
		235				240					245					
gac	gac	cct	tac	gag	gca	cca	gtg	aat	tgc	gag	gta	gtg	ctg	aaa	cac	820
Asp	Asp	Pro	Tyr	Glu	Ala	Pro	Val	Asn	Cys	Glu	Val	Val	Leu	Lys	His	
	250				255					260					265	
aca	gga	gac	gac	gag	tcg	tgt	tcg	cca	cgt	cag	atg	gct	gag	aac	atc	868
Thr	Gly	Asp	Asp	Glu	Ser	Cys	Ser	Pro	Arg	Gln	Met	Ala	Glu	Asn	Ile	

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                270                275                280
atc tct tac ctg caa aac aaa ggt tat ctt gag ggc taa gtcaaagtcg      917
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Phe Leu Lys Leu Pro Ala Ser Ser Ile Pro Ala Asp Ser Arg Lys Leu
              35              40              45
Val Ala Asn Ser Thr Ser Phe His Pro Ile Ser Ala Val Asn Val Ser
              50              55              60
Ala Gln Ala Ser Leu Thr Ala Asp Phe Pro Ala Leu Ser Glu Thr Ile
              65              70              75              80
Leu Lys Glu Gly Arg Asn Asn Gly Lys Glu Lys Ala Glu Asn Ile Val
              85              90              95
Trp His Glu Ser Ser Ile Cys Arg Cys Asp Arg Gln Gln Leu Leu Gln
              100             105             110
Gln Lys Gly Cys Val Val Trp Ile Thr Gly Leu Ser Gly Ser Gly Lys
              115             120             125
Ser Thr Val Ala Cys Ala Leu Ser Lys Ala Leu Phe Glu Arg Gly Lys
              130             135             140
Leu Thr Tyr Thr Leu Asp Gly Asp Asn Val Arg His Gly Leu Asn Arg
              145             150             155             160
Asp Leu Thr Phe Lys Ala Glu His Arg Thr Glu Asn Ile Arg Arg Ile
              165             170             175
Gly Glu Val Ala Lys Leu Phe Ala Asp Val Gly Val Ile Cys Ile Ala
              180             185             190
Ser Leu Ile Ser Pro Tyr Arg Arg Asp Arg Asp Ala Cys Arg Ser Leu
              195             200             205
Leu Pro Asp Gly Asp Phe Val Glu Val Phe Met Asp Val Pro Leu His
              210             215             220

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Val Cys Glu Ser Arg Asp Pro Lys Gly Leu Tyr Lys Leu Ala Arg Ala  
 225 230 235 240

Gly Lys Ile Lys Gly Phe Thr Gly Ile Asp Asp Pro Tyr Glu Ala Pro  
 245 250 255

Val Asn Cys Glu Val Val Leu Lys His Thr Gly Asp Asp Glu Ser Cys  
 260 265 270

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Gly Tyr Leu Glu Gly  
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tca gga gcg agt acg aag tat gac gcc aaa gat ata gga agt ctt ggg 99  
 Ser Gly Ala Ser Thr Lys Tyr Asp Ala Lys Asp Ile Gly Ser Leu Gly  
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 Ser Lys Ala Ser Ser Val Ser Val Arg Pro Ser Pro Arg Thr Glu Gly  
 30 35 40 45

gag atc tta cag tct cca aat ctc aag agt ttt agc ttt gct gag ctt 195  
 Glu Ile Leu Gln Ser Pro Asn Leu Lys Ser Phe Ser Phe Ala Glu Leu  
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aaa tca gca acc agg aat ttt aga cca gac agt gtg ctt ggt gaa ggt 243  
 Lys Ser Ala Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly  
 65 70 75

gga ttc ggt tgt gtt ttc aaa gga tgg att gat gag aag tct ctc act 291  
 Gly Phe Gly Cys Val Phe Lys Gly Trp Ile Asp Glu Lys Ser Leu Thr  
 80 85 90

gcc tca aga cca ggc acg ggt ttg gtt att gcc gtc aaa aag ctt aac 339  
 Ala Ser Arg Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn  
 95 100 105

caa gat ggt tgg caa ggt cac cag gag tgg ctg gct gaa gtg aat tac 387  
 Gln Asp Gly Trp Gln Gly His Gln Glu Trp Leu Ala Glu Val Asn Tyr

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ctt ggt cag ttt tct cac cgt cac ctt gtg aag ctg att ggt tat tgc				435
Leu Gly Gln Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys	130	135	140	
cta gag gat gag cac cgt ctt ctt gtt tac gag ttc atg cct cgg ggt				483
Leu Glu Asp Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly	145	150	155	
agc ttg gag aat cat ctt ttc agg aga ggt ttg tac ttc caa ccg tta				531
Ser Leu Glu Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu	160	165	170	
tct tgg aaa ctt cgg ttg aaa gtt gct ctt ggt gct gca aag gga ctt				579
Ser Trp Lys Leu Arg Leu Lys Val Ala Leu Gly Ala Ala Lys Gly Leu	175	180	185	
gct ttt ctt cac agt tcc gag aca aga gtg ata tac cga gat ttc aag				627
Ala Phe Leu His Ser Ser Glu Thr Arg Val Ile Tyr Arg Asp Phe Lys	190	195	200	205
act tct aat atc ctt ctt gac tcg gag tac aac gca aag ctt tct gat				675
Thr Ser Asn Ile Leu Leu Asp Ser Glu Tyr Asn Ala Lys Leu Ser Asp	210	215	220	
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Phe Gly Leu Ala Lys Asp Gly Pro Ile Gly Asp Lys Ser His Val Ser	225	230	235	
aca cga gtc atg ggt aca cac gga tat gca gct cct gaa tac ctt gca				771
Thr Arg Val Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala	240	245	250	
acc ggt cat cta aca aca aag agt gat gtc tat agc ttc ggg gtt gtc				819
Thr Gly His Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe Gly Val Val	255	260	265	
ctt ctg gag ctg ttg tct ggt cgt cga gca gtg gac aag aac cgc cca				867
Leu Leu Glu Leu Leu Ser Gly Arg Arg Ala Val Asp Lys Asn Arg Pro	270	275	280	285
tct gga gag agg aac ctt gtg gag tgg gct aaa cca tac ctc gta aac				915
Ser Gly Glu Arg Asn Leu Val Glu Trp Ala Lys Pro Tyr Leu Val Asn	290	295	300	
aaa aga aag ata ttc cga gtc att gat aat cgt ctt cag gac cag tac				963
Lys Arg Lys Ile Phe Arg Val Ile Asp Asn Arg Leu Gln Asp Gln Tyr	305	310	315	
tct atg gaa gaa gca tgt aaa gtg gct act ctg tct ctg aga tgt ctc				1011
Ser Met Glu Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu	320	325	330	
acc aca gag att aag ctg aga cca aac atg agc gag gtt gtt tcg cac				1059
Thr Thr Glu Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His	335	340	345	

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aaa aca gat aga aga atg cgt agg aga agt gac agt gtt gtc agc aaa 1155
Lys Thr Asp Arg Arg Met Arg Arg Arg Ser Asp Ser Val Val Ser Lys
370 375 380

aaa gtg aat gca ggt ttt gct cga cag act gct gtt ggc agt aca gtt 1203
Lys Val Asn Ala Gly Phe Ala Arg Gln Thr Ala Val Gly Ser Thr Val
385 390 395

gtt gct tat cct cgc cca tca gcc tgc cca ctg tat gtt tga 1245
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Gln Ser Pro Asn Leu Lys Ser Phe Ser Phe Ala Glu Leu Lys Ser Ala
 50 55 60

Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly Gly Phe Gly
 65 70 75 80

Cys Val Phe Lys Gly Trp Ile Asp Glu Lys Ser Leu Thr Ala Ser Arg
 85 90 95

Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn Gln Asp Gly
 100 105 110

Trp Gln Gly His Gln Glu Trp Leu Ala Glu Val Asn Tyr Leu Gly Gln
 115 120 125

Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys Leu Glu Asp
 130 135 140

Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly Ser Leu Glu
 145 150 155 160

Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu Ser Trp Lys

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Leu Arg Leu Lys Val Ala Leu Gly Ala Ala Lys Gly Leu Ala Phe Leu	180	185	190		
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Ile Leu Leu Asp Ser Glu Tyr Asn Ala Lys Leu Ser Asp Phe Gly Leu	210	215	220		
Ala Lys Asp Gly Pro Ile Gly Asp Lys Ser His Val Ser Thr Arg Val	225	230	235	240	
Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala Thr Gly His	245	250	255		
Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe Gly Val Val Leu Leu Glu	260	265	270		
Leu Leu Ser Gly Arg Arg Ala Val Asp Lys Asn Arg Pro Ser Gly Glu	275	280	285		
Arg Asn Leu Val Glu Trp Ala Lys Pro Tyr Leu Val Asn Lys Arg Lys	290	295	300		
Ile Phe Arg Val Ile Asp Asn Arg Leu Gln Asp Gln Tyr Ser Met Glu	305	310	315	320	
Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu Thr Thr Glu	325	330	335		
Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His Leu Glu His	340	345	350		
Ile Gln Ser Leu Asn Ala Ala Ile Gly Gly Asn Met Asp Lys Thr Asp	355	360	365		
Arg Arg Met Arg Arg Arg Ser Asp Ser Val Val Ser Lys Lys Val Asn	370	375	380		
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 Met Leu Glu Lys Lys Leu Ala Ala Ala Glu Val Ser Glu Glu  
 1 5 10

gag caa aat aac ttg cta aag gat ttg gag atg aag gaa act gaa tat 158  
 Glu Gln Asn Asn Leu Leu Lys Asp Leu Glu Met Lys Glu Thr Glu Tyr  
 15 20 25 30

atg cgc cgt cag agg cat aaa atg gga gct gat gac ttt gag cca ttg 206

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Thr Met Ile Gly Lys Gly Ala Phe Gly Glu
      50              55

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tcaaaaaagt atggcatgct aatttttctc tttctctttg cag gtt agg atc tgt 431
                        Val Arg Ile Cys
                        60

agg gag aag gga aca ggc aat gtc tat gca atg aag aag ctt aag aaa 479
Arg Glu Lys Gly Thr Gly Asn Val Tyr Ala Met Lys Lys Leu Lys Lys
      65              70              75

tct gag atg ctt cgc aga ggc cag gta tttaaattcc ttcaagtggc 526
Ser Glu Met Leu Arg Arg Gly Gln Val
      80              85

tttcgtttga catttgttta gttgggtgat gtgaatgtgg aatctgattt tcag gtg 583
                        Val

gaa cat gta aaa gca gag aga aat tta ctt gca gaa gtt gat agc aat 631
Glu His Val Lys Ala Glu Arg Asn Leu Leu Ala Glu Val Asp Ser Asn
      90              95              100

tgc att gtc aaa ctg tat tgt tct ttc caa gat gaa gag tac ttg tat 679
Cys Ile Val Lys Leu Tyr Cys Ser Phe Gln Asp Glu Glu Tyr Leu Tyr
      105              110              115

ctc ata atg gag tat tta cct ggt ggg gat atg atg act tta ctt atg 727
Leu Ile Met Glu Tyr Leu Pro Gly Gly Asp Met Met Thr Leu Leu Met
      120              125              130

agg aaa gac acc ctc act gaa gac gag gcc agg ttt tat att ggg gaa 775
Arg Lys Asp Thr Leu Thr Glu Asp Glu Ala Arg Phe Tyr Ile Gly Glu
      135              140              145              150

act gtc ctg gct att gag tcc att cat aag cac aac tac att cac ag 822
Thr Val Leu Ala Ile Glu Ser Ile His Lys His Asn Tyr Ile His Ar
      155              160              165

gtcagtgaag cagaatatat gatttagttc tagctcccat tggtattttg ttctaaacgt 882

ctttttttct ccaatgtgat acag a gat atc aag cct gat aat ctg cta ctt 934
                        g Asp Ile Lys Pro Asp Asn Leu Leu
                        s              170              175

gac aaa gac ggc cac atg aaa ttg tca gat ttt gga tta tgt aaa cca 982
Asp Lys Asp Gly His Met Lys Leu Ser Asp Phe Gly Leu Cys Lys Pro
      180              185              190

tta gac tgt agt aat ctt caa gag aaa gac ttt aca gtt gca aga aac 1030

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Leu Asp Cys Ser Asn Leu Gln Glu Lys Asp Phe Thr Val Ala Arg Asn  
 195 200 205  
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 Val Ser Gly Ala Leu Gln Ser Asp Gly Arg Pro Val Ala Thr Arg Arg  
 210 215 220  
 acc caa caa gag caa tta cta aac tgg cag aga aat aga agg atg ctt 1126  
 Thr Gln Gln Glu Gln Leu Leu Asn Trp Gln Arg Asn Arg Arg Met Leu  
 225 230 235  
 gtaagtttca cttattcctc atcttttctt ccagagatgt ggagtagtcc acagtatcca 1186  
 gtatatttctg ttattgaaag caaattctct ccattgatat agacatctat gttagatatg 1246  
 acttactagg ttaaggtcat tacttttcag gct tat tcc aca gtt ggc act cct 1299  
 Ala Tyr Ser Thr Val Gly Thr Pro  
 240 245  
 gac tat att gcc cca gaa gtt ctg ttg aaa aaa gga tat gga atg gaa 1347  
 Asp Tyr Ile Ala Pro Glu Val Leu Leu Lys Lys Gly Tyr Gly Met Glu  
 250 255 260  
 tgt gat tg gtaggtgaag ccaacctatt cctatttgtg gtcttttgatt tcttttgtgt 1405  
 Cys Asp Trp  
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 aaataaataa tatgggtgaa taatcttgag atttag g tgg tct ctt ggc gcc att 1460  
 p Trp Ser Leu Gly Ala Ile  
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 atg tat gaa atg ctt gtg ggg ttt ccg ccc ttt tat tca gat gac cca 1508  
 Met Tyr Glu Met Leu Val Gly Phe Pro Pro Phe Tyr Ser Asp Asp Pro  
 275 280 285  
 atg aca act tgt agg aag gtaattaatc cattcctttt tgaatctttc 1556  
 Met Thr Thr Cys Arg Lys  
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 tatgcag ata gta aat tgg aga aat tac ttg aaa ttc cca gat gag gtt 1725  
 Ile Val Asn Trp Arg Asn Tyr Leu Lys Phe Pro Asp Glu Val  
 295 300 305  
 aga cta tca cca gaa gcc aag gat ctt att tgt agg ctt tta tgc aat 1773  
 Arg Leu Ser Pro Glu Ala Lys Asp Leu Ile Cys Arg Leu Leu Cys Asn  
 310 315 320  
 gtt gaa caa agg ctt gga aca aaa gga gca gat gaa att aag 1815  
 Val Glu Gln Arg Leu Gly Thr Lys Gly Ala Asp Glu Ile Lys  
 325 330 335  
 gtgtgtgatg cgttgttcaa ctttgagatt caaagttccc ttatgtaaga tcattgtgtg 1875

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caattcttaa aaacgatttg actggtttct ttcag ggt cac cct tgg ttt aga 1928
                                Gly His Pro Trp Phe Arg
                                340

ggc aca gaa tgg gga aaa ttg tat caa atg aaa gct gcc ttt att ccc 1976
Gly Thr Glu Trp Gly Lys Leu Tyr Gln Met Lys Ala Ala Phe Ile Pro
345                                350                                355                                360

caa gtt aat gat gag ttg gac acc caa aat ttt gag aaa ttt gaa gag 2024
Gln Val Asn Asp Glu Leu Asp Thr Gln Asn Phe Glu Lys Phe Glu Glu
                                365                                370                                375

gtaacacact gatactatca gctaattgat tctatagtga aatattggtg caatatatgc 2084

caccaaatga tgtggcatga tgtatatact gaaatattgg tatcacagat gattttttatg 2144

ctcctgataa ggaaaataat gtatactctt ctttgattcc ttctggaaca g act gac 2201
                                Thr Asp

aag caa gtt cca aag tca gcc aag tca ggt cca tgg aga aag 2243
Lys Gln Val Pro Lys Ser Ala Lys Ser Gly Pro Trp Arg Lys
                                380                                385                                390

gtacagcata agcactgact ttttggcatt atgtaccatc aagctttttt tttttatcta 2303

atagaagagt gatcatactt caaaatttat ctataagtgg gttccttgag atatgttggt 2363

ctttgatgat actacagacg tagcttaaaa tattacatgc aacaaagagc tcagaatgat 2423

gaaattggct cagtttctgt cacaggcggt tctatctttg tactatattc acaaaaacgt 2483

gattcactct tttaggttca aattttctta tggtaattta gaatttggag ctgattggga 2543

tgctactaac agaattatgt tgtaaatctg ccagttctgc atgttgacgt gtgtagatg 2603

aatcacttat ctttttggac caacatgata taacttagaa cctgttctgt caatagaatt 2663

tatgtcatga accaaaagga ttcttgtgaa tttcataaca tgacgctggc tttctttttt 2723

ttttctccag atg ctc tca tcc aaa gac att aac ttt gtt ggt tat act 2772
                                Met Leu Ser Ser Lys Asp Ile Asn Phe Val Gly Tyr Thr
                                395                                400                                405

tac aag aac gta gaa atc gta aat gat gac caa ata cca ggg ata g 2818
Tyr Lys Asn Val Glu Ile Val Asn Asp Asp Gln Ile Pro Gly Ile A
                                410                                415                                420

gtaattcact taacccccct tccgttgctg aggaagaagc aacaatacta gattaccttg 2878

tgattatcat cgcattgttg ctgcatttgt aatttgtttt attgtgcag ct gag ttg 2935
                                la Glu Leu
                                G

aag aag aag agc aat aag cca aaa agg ccg tct att aaa tct ctc ttt g 2984
Lys Lys Lys Ser Asn Lys Pro Lys Arg Pro Ser Ile Lys Ser Leu Phe G
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Arg Gln Arg His Lys Met Gly Ala Asp Asp Phe Glu Pro Leu Thr Met
      35             40             45
Ile Gly Lys Gly Ala Phe Gly Glu Val Arg Ile Cys Arg Glu Lys Gly
      50             55             60
Thr Gly Asn Val Tyr Ala Met Lys Lys Leu Lys Lys Ser Glu Met Leu
      65             70             75             80
Arg Arg Gly Gln Val Val Glu His Val Lys Ala Glu Arg Asn Leu Leu
      85             90             95
Ala Glu Val Asp Ser Asn Cys Ile Val Lys Leu Tyr Cys Ser Phe Gln
      100            105            110
Asp Glu Glu Tyr Leu Tyr Leu Ile Met Glu Tyr Leu Pro Gly Gly Asp
      115            120            125
Met Met Thr Leu Leu Met Arg Lys Asp Thr Leu Thr Glu Asp Glu Ala
      130            135            140
Arg Phe Tyr Ile Gly Glu Thr Val Leu Ala Ile Glu Ser Ile His Lys
      145            150            155            160
His Asn Tyr Ile His Arg Asp Ile Lys Pro Asp Asn Leu Leu Leu Asp
      165            170            175
Lys Asp Gly His Met Lys Leu Ser Asp Phe Gly Leu Cys Lys Pro Leu

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180										185					190				
Asp	Cys	Ser	Asn	Leu	Gln	Glu	Lys	Asp	Phe	Thr	Val	Ala	Arg	Asn	Val				
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Ser	Gly	Ala	Leu	Gln	Ser	Asp	Gly	Arg	Pro	Val	Ala	Thr	Arg	Arg	Thr				
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Gln	Gln	Glu	Gln	Leu	Leu	Asn	Trp	Gln	Arg	Asn	Arg	Arg	Met	Leu	Ala				
225					230					235					240				
Tyr	Ser	Thr	Val	Gly	Thr	Pro	Asp	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Leu				
				245					250					255					
Lys	Lys	Gly	Tyr	Gly	Met	Glu	Cys	Asp	Trp	Trp	Ser	Leu	Gly	Ala	Ile				
			260					265					270						
Met	Tyr	Glu	Met	Leu	Val	Gly	Phe	Pro	Pro	Phe	Tyr	Ser	Asp	Asp	Pro				
		275					280						285						
Met	Thr	Thr	Cys	Arg	Lys	Ile	Val	Asn	Trp	Arg	Asn	Tyr	Leu	Lys	Phe				
	290					295					300								
Pro	Asp	Glu	Val	Arg	Leu	Ser	Pro	Glu	Ala	Lys	Asp	Leu	Ile	Cys	Arg				
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Leu	Leu	Cys	Asn	Val	Glu	Gln	Arg	Leu	Gly	Thr	Lys	Gly	Ala	Asp	Glu				
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Ile	Lys	Gly	His	Pro	Trp	Phe	Arg	Gly	Thr	Glu	Trp	Gly	Lys	Leu	Tyr				
			340					345					350						
Gln	Met	Lys	Ala	Ala	Phe	Ile	Pro	Gln	Val	Asn	Asp	Glu	Leu	Asp	Thr				
		355					360					365							
Gln	Asn	Phe	Glu	Lys	Phe	Glu	Glu	Thr	Asp	Lys	Gln	Val	Pro	Lys	Ser				
	370					375					380								
Ala	Lys	Ser	Gly	Pro	Trp	Arg	Lys	Met	Leu	Ser	Ser	Lys	Asp	Ile	Asn				
385					390					395					400				
Phe	Val	Gly	Tyr	Thr	Tyr	Lys	Asn	Val	Glu	Ile	Val	Asn	Asp	Asp	Gln				
				405					410					415					
Ile	Pro	Gly	Ile	Ala	Glu	Leu	Lys	Lys	Lys	Ser	Asn	Lys	Pro	Lys	Arg				
			420				425						430						
Pro	Ser	Ile	Lys	Ser	Leu	Phe	Glu	Asp	Glu	Thr	Ser	Gly	Gly	Thr	Thr				
		435					440					445							
Thr	His	Gln	Gly	Ser	Phe	Leu	Asn	Leu	Leu	Pro	Thr	Gln	Ile	Glu	Asp				
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atg aac ggt gac gaa tgc gcg aac gtt gcg acg tgc tgg gtt act tct 102
Met Asn Gly Asp Glu Cys Ala Asn Val Ala Thr Cys Trp Val Thr Ser
 10                               15                               20                               25

cta gct tgt gta gtt gac gcc gga cga tat acg aaa aag gta tcc cac 150
Leu Ala Cys Val Val Asp Ala Gly Arg Tyr Thr Lys Lys Val Ser His
                               30                               35                               40

gac cgg cga acg agg tgg ccc gcc tgg aaa gca cga cgg gat cgt cat 198
Asp Arg Arg Thr Arg Trp Pro Ala Trp Lys Ala Arg Arg Asp Arg His
                               45                               50                               55

agt gtc cga agt gat agc ggc cta gac agt cat gca ctt gaa ggt gga 246
Ser Val Arg Ser Asp Ser Gly Leu Asp Ser His Ala Leu Glu Gly Gly
                               60                               65                               70

aaa cga cgt gag tca tgc gta tca cta gct cac gaa cga gat tat gca 294
Lys Arg Arg Glu Ser Cys Val Ser Leu Ala His Glu Arg Asp Tyr Ala
                               75                               80                               85

cta acg gca cgg tgg gat cgt agc att gca atg acg gat gac acg aac 342
Leu Thr Ala Arg Trp Asp Arg Ser Ile Ala Met Thr Asp Asp Thr Asn
 90                               95                               100                               105

cca caa acc caa cgt aaa ttt gag aaa cat act cgg gat gta gaa gct 390
Pro Gln Thr Gln Arg Lys Phe Glu Lys His Thr Arg Asp Val Glu Ala
                               110                               115                               120

gtt cga ttt tct cca cga gat cgt cta att gta tct gcg ggt gca gat 438
Val Arg Phe Ser Pro Arg Asp Arg Leu Ile Val Ser Ala Gly Ala Asp
                               125                               130                               135

ggg gta att gca gta tgt ccg gtt gct ggt gaa tgt gat gat gac gat 486
Gly Val Ile Ala Val Cys Pro Val Ala Gly Glu Cys Asp Asp Asp Asp
                               140                               145                               150

gcc cgt gat ggt cat gaa gat tgt gtt agt agt att tgc ttt tca cca 534
Ala Arg Asp Gly His Glu Asp Cys Val Ser Ser Ile Cys Phe Ser Pro
                               155                               160                               165

tca cta gaa cac ccg atc ctc ttt tct ggt agt tgt atc tac ttt att 582
Ser Leu Glu His Pro Ile Leu Phe Ser Gly Ser Cys Ile Tyr Phe Ile

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170              175              180              185
aaa gtg tgg aat gtc aat gga aag aaa tgt agg acg ccg cta aaa aag 630
Lys Val Trp Asn Val Asn Gly Lys Lys Cys Arg Thr Pro Leu Lys Lys
              190              195              200

cat agt aat ccc gta tct aca cgg aca cag tca gaa gag gga agg cta 678
His Ser Asn Pro Val Ser Thr Arg Thr Gln Ser Glu Glu Gly Arg Leu
              205              210              215

tgt gca aaa ggt ggt aaa agc ggt gca cgg cta cta ccc gat cta agt 726
Cys Ala Lys Gly Gly Lys Ser Gly Ala Arg Leu Leu Pro Asp Leu Ser
              220              225              230

act cag gaa caa cta ccc aaa att aat caa gaa aac cct att aat caa 774
Thr Gln Glu Gln Leu Pro Lys Ile Asn Gln Glu Asn Pro Ile Asn Gln
              235              240              245

att gct ttt tca cct agt ccg ttc gtc gtc acg tgc caa acg gaa aga 822
Ile Ala Phe Ser Pro Ser Pro Phe Val Val Thr Cys Gln Thr Glu Arg
250              255              260              265

tcc cta tct caa acg tgg tga ccgtgcaccg gcacgggtgaa aaagtcgacc 873
Ser Leu Ser Gln Thr Trp
              270

ggatcgaccg accgaaagcc tgctcgctgg acaaaaaaag agcttttttag gcctttcgct 933

ttttttgaag aaaaaaggct cgcgaaaaaa aaaaagctcg aaatca 979

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Gly Arg Tyr Thr Lys Lys Val Ser His Asp Arg Arg Thr Arg Trp Pro
              35              40              45

Ala Trp Lys Ala Arg Arg Asp Arg His Ser Val Arg Ser Asp Ser Gly
              50              55              60

Leu Asp Ser His Ala Leu Glu Gly Gly Lys Arg Arg Glu Ser Cys Val
              65              70              75              80

Ser Leu Ala His Glu Arg Asp Tyr Ala Leu Thr Ala Arg Trp Asp Arg
              85              90              95

Ser Ile Ala Met Thr Asp Asp Thr Asn Pro Gln Thr Gln Arg Lys Phe
              100              105              110

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Glu Lys His Thr Arg Asp Val Glu Ala Val Arg Phe Ser Pro Arg Asp  
 115 120 125  
 Arg Leu Ile Val Ser Ala Gly Ala Asp Gly Val Ile Ala Val Cys Pro  
 130 135 140  
 Val Ala Gly Glu Cys Asp Asp Asp Ala Arg Asp Gly His Glu Asp  
 145 150 155 160  
 Cys Val Ser Ser Ile Cys Phe Ser Pro Ser Leu Glu His Pro Ile Leu  
 165 170 175  
 Phe Ser Gly Ser Cys Ile Tyr Phe Ile Lys Val Trp Asn Val Asn Gly  
 180 185 190  
 Lys Lys Cys Arg Thr Pro Leu Lys Lys His Ser Asn Pro Val Ser Thr  
 195 200 205  
 Arg Thr Gln Ser Glu Glu Gly Arg Leu Cys Ala Lys Gly Gly Lys Ser  
 210 215 220  
 Gly Ala Arg Leu Leu Pro Asp Leu Ser Thr Gln Glu Gln Leu Pro Lys  
 225 230 235 240  
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 Met Lys Arg Leu Ser  
 1 5

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agc tca gat tca atg tgt ggt cta atc tcc act tct aca g gttcttatta 165
Ser Ser Asp Ser Met Cys Gly Leu Ile Ser Thr Ser Thr A
      10                      15

ccatctttgt tctttctact ttttgctaat gtcagacaaa acccatgtga tcctttcttc 225

actttccact gtttctttta ttgacaag at tca ttt ggt tac aca aca gat gaa 279
                        sp Ser Phe Gly Tyr Thr Thr Asp Glu
                        20                      25

cag agt cca aga ggg tac gga agt aat tac caa tct atg ctt gaa ggt 327
Gln Ser Pro Arg Gly Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly
      30                      35                      40

tac gat gaa gat gct aca cta atc gag gaa tat tcc ggc aac cac cac 375
Tyr Asp Glu Asp Ala Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His
      45                      50                      55

cac atg ggt cta tcg gag aag aag aga aga tta aaa gtt gac caa gtc 423
His Met Gly Leu Ser Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val
      60                      65                      70                      75

aaa gct ctt gag aag aat ttc gaa ctt gag aat aaa ctc gaa cct gag 471
Lys Ala Leu Glu Lys Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu
      80                      85                      90

agg aaa act aaa tta gca caa gag ctt gga ctt caa cct cgt caa gta 519
Arg Lys Thr Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val
      95                      100                      105

gct gtt tgg ttt cag aac cgt cgt gca cgg tgg aaa aca aaa cag ctt 567
Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu
      110                      115                      120

gaa aaa gat tac ggt gtt ctt aag ggt caa tac gat tct ctc cgc cac 615
Glu Lys Asp Tyr Gly Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His
      125                      130                      135

aat ttc gat tct ctc cgc cgt gac aat gat tcc ctt ctc caa gag 660
Asn Phe Asp Ser Leu Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu
      140                      145                      150

gtacaatatt agagacttta aaccataaaa attgaaactt cagagacgaa aatgcaaaaa 720

ggtttgattt ttaaagtttt tggttgacag att agt aaa atc aaa gct aag gta 773
                        Ile Ser Lys Ile Lys Ala Lys Val
                        155                      160

aac ggt gaa gaa gat aac aac aac aac aaa gct att acg gag ggt gtt 821
Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu Gly Val
      165                      170                      175

aag gaa gag gaa gtt cac aag acg gat tcg att cct tcg tct cct ctg 869
Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser Pro Leu
      180                      185                      190

cag ttt cta gaa cat tcc tct ggt ttt aac tac cgg cga agc ttc act 917

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 195 200 205 210  
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 Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala Gly Ser  
 215 220 225  
 tcc gat agt tgc gat tca agc gcc gtt ctt aac gac gaa aca agt tct 1013  
 Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr Ser Ser  
 230 235 240  
 gat aac gga aga ttg acg ccg cct gtg acg gtt act ggc ggg agt ttc 1061  
 Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly Ser Phe  
 245 250 255  
 tta cag ttt gtg aaa aca gag caa aca gag gat cac gag gat ttt cta 1109  
 Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp Phe Leu  
 260 265 270  
 agc ggt gaa gaa gct tgt ggt ttc ttc tcc gat gaa cag ccg ccg tca 1157  
 Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser  
 275 280 285 290  
 ctt cat tgg tac tct gct tca gat cat tgg act tga gaattgttta 1203  
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 35 40 45  
 Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His His Met Gly Leu Ser  
 50 55 60  
 Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val Lys Ala Leu Glu Lys  
 65 70 75 80  
 Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr Lys Leu  
 85 90 95  
 Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp Phe Gln  
 100 105 110

Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp Tyr Gly  
           115  120  125  
 Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His Asn Phe Asp Ser Leu  
           130  135  140  
 Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu Ile Ser Lys Ile Lys Ala  
 145  150  155  160  
 Lys Val Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu  
   165  170  175  
 Gly Val Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser  
   180  185  190  
 Pro Leu Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser  
           195  200  205  
 Phe Thr Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala  
           210  215  220  
 Gly Ser Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr  
 225  230  235  240  
 Ser Ser Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly  
   245  250  255  
 Ser Phe Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp  
   260  265  270  
 Phe Leu Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro  
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 <222> (22)..(1122)

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 Ser Ser Ile Arg Trp Phe Ala Asn Arg Leu Val Ser Gly Ser Leu Leu  
   15  20  25  
 ttg tgt gct aac gcc tac agt cgt cgt act ccc gcg tcc ggg gcc gca 147

Leu Cys Ala Asn Ala Tyr Ser Arg Arg Thr Pro Ala Ser Gly Ala Ala	
30 35 40	
tta cag cag atg aac cgt gcc agt cag tca gtg aat tac cga cga cgt	195
Leu Gln Gln Met Asn Arg Ala Ser Gln Ser Val Asn Tyr Arg Arg Arg	
45 50 55	
gag ctg tca tta atc agc ggc cgg aaa cag ggt gtc cag tct ctg ggt	243
Glu Leu Ser Leu Ile Ser Gly Arg Lys Gln Gly Val Gln Ser Leu Gly	
60 65 70	
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Tyr Arg Leu Ala Arg Leu Asp Asn Arg Ala Leu Ala Gln Leu Leu His	
75 80 85 90	
agg gat ggc cag ccc gag gaa gtg gta cag cgc ggc aat gaa atc agc	339
Arg Asp Gly Gln Pro Glu Glu Val Val Gln Arg Gly Asn Glu Ile Ser	
95 100 105	
tat ttc gaa acg gga ctt gaa ccg acc acg ctt aga cgt gtg cgc gat	387
Tyr Phe Glu Thr Gly Leu Glu Pro Thr Thr Leu Arg Arg Val Arg Asp	
110 115 120	
tgt gtt gtt gcc gct ctg cca acc gtt atc tat acc gga ttc aaa cgt	435
Cys Val Val Ala Ala Leu Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg	
125 130 135	
gtt tct cct tac tac gaa ttt atc tcc gtc ggg cgc acg agg gtt gct	483
Val Ser Pro Tyr Tyr Glu Phe Ile Ser Val Gly Arg Thr Arg Val Ala	
140 145 150	
gat cgt ctt agc gaa gtc acg caa gtg gtt ccc cga gat gat aca cgc	531
Asp Arg Leu Ser Glu Val Thr Gln Val Val Pro Arg Asp Asp Thr Arg	
155 160 165 170	
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Tyr Val Tyr Ile Val Trp Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala	
175 180 185	
cgg ggg gat ctc cgt gat cgc gat ggt gaa acg ctg gaa aag ttt cgc	627
Arg Gly Asp Leu Arg Asp Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg	
190 195 200	
gtg att gct ttt aac gtc acg ctg gat atc agc agc agt atg gag ccg	675
Val Ile Ala Phe Asn Val Thr Leu Asp Ile Ser Ser Ser Met Glu Pro	
205 210 215	
ctg gcg aag gga gat ttg ccg ccg ttg ctt gct gtt cct gta ggt gaa	723
Leu Ala Lys Gly Asp Leu Pro Pro Leu Leu Ala Val Pro Val Gly Glu	
220 225 230	
caa gct aga ttc agc ttg acg cca acc tgg ttg cca cag ggt cgt agc	771
Gln Ala Arg Phe Ser Leu Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser	
235 240 245 250	
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Asp Val Ser Ser Ser Arg Arg Gly Leu Pro Arg Met Asp Lys Val Pro	

255	260	265	
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Ile Glu Ser Arg Leu Ser Thr Asp Gly Val Phe Ser Phe Ser Val Asn			
270	275	280	
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Val Asn Gly Ala Thr Pro Ser Arg Trp Asp Gln Met Leu Arg Thr Gly			
285	290	295	
cgc agg ccc gtc agt aga agc gta cgt gat gtc gcc gaa aac acc att			963
Arg Arg Pro Val Ser Arg Ser Val Arg Asp Val Ala Glu Asn Thr Ile			
300	305	310	
ggc ggt gaa ctg ccg ccg cgt agc tgc tcg cga ccc gat ccg ttg acc			1011
Gly Gly Glu Leu Pro Pro Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr			
315	320	325	330
gct gac cgc cga cgc tgc gct agc ctg agc ctg ccc agc ctg cca gct			1059
Ala Asp Arg Arg Arg Cys Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala			
335	340	345	
cga cag ccc tcc caa acg gag aaa cgc att gtc gag aat att aag tac			1107
Arg Gln Pro Ser Gln Thr Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr			
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Gly Ala Ala Pro			
365			

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&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 76

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Ser Arg Arg Thr Pro Ala Ser Gly Ala Ala Leu Gln Gln Met Asn Arg
35 40 45

Ala Ser Gln Ser Val Asn Tyr Arg Arg Arg Glu Leu Ser Leu Ile Ser
50 55 60

Gly Arg Lys Gln Gly Val Gln Ser Leu Gly Tyr Arg Leu Ala Arg Leu
65 70 75 80

Asp Asn Arg Ala Leu Ala Gln Leu Leu His Arg Asp Gly Gln Pro Glu
85 90 95

Glu Val Val Gln Arg Gly Asn Glu Ile Ser Tyr Phe Glu Thr Gly Leu
100 105 110

Glu Pro Thr Thr Leu Arg Arg Val Arg Asp Cys Val Val Ala Ala Leu  
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 Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg Val Ser Pro Tyr Tyr Glu  
 130 135 140  
 Phe Ile Ser Val Gly Arg Thr Arg Val Ala Asp Arg Leu Ser Glu Val  
 145 150 155 160  
 Thr Gln Val Val Pro Arg Asp Asp Thr Arg Tyr Val Tyr Ile Val Trp  
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 Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala Arg Gly Asp Leu Arg Asp  
 180 185 190  
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 195 200 205  
 Thr Leu Asp Ile Ser Ser Ser Met Glu Pro Leu Ala Lys Gly Asp Leu  
 210 215 220  
 Pro Pro Leu Leu Ala Val Pro Val Gly Glu Gln Ala Arg Phe Ser Leu  
 225 230 235 240  
 Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser Asp Val Ser Ser Ser Arg  
 245 250 255  
 Arg Gly Leu Pro Arg Met Asp Lys Val Pro Ile Glu Ser Arg Leu Ser  
 260 265 270  
 Thr Asp Gly Val Phe Ser Phe Ser Val Asn Val Asn Gly Ala Thr Pro  
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 Ser Arg Trp Asp Gln Met Leu Arg Thr Gly Arg Arg Pro Val Ser Arg  
 290 295 300  
 Ser Val Arg Asp Val Ala Glu Asn Thr Ile Gly Gly Glu Leu Pro Pro  
 305 310 315 320  
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Leu Glu Gly Asp Phe Asn Lys Asp Asn Thr Ser Ser Ala Thr Glu Ile																						
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gat act tta gag aac tta gat gac act agg cag ata agt aaa gga aaa																						149
Asp Thr Leu Glu Asn Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys																						
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cct ccg agg cac ctc aca agc agt gct act agg ctg cag ctt gca gcc																						197
Pro Pro Arg His Leu Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala																						
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aat gcg gtaatatct tgaccctgct tttctttttt cttttctttt gttacaatgg																						253
Asn Ala																						
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		Asp Val Asp Val Cys Asn																				
		65																				
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Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu Pro Val Tyr																						
		70				75				80												
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Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe Met Glu Asp																						
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gaa cac att tgc atc gat gat ctt gtt aat cat ctt ggt gca gct att																						452
Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly Ala Ala Ile																						
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caa tgc tct tct ctt gga gcc ttc tat ggg gtgagtttat cttccaatct																						502
Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly																						
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actagtagca tataagaggt attacttcaa aaactcttct aacatttggt gattgtgtgt 622

cctttggcag gta ttt gat ggc cac ggt ggc aca gat gca gca cac ttt 671  
 Val Phe Asp Gly His Gly Gly Thr Asp Ala Ala His Phe  
 130 135

gtt aga aag aac att ctg aga ttc att gta gag gac tcc tcc ttc cca 719  
 Val Arg Lys Asn Ile Leu Arg Phe Ile Val Glu Asp Ser Ser Phe Pro  
 140 145 150

cta tgc gta aag aaa gca att aag agt gct ttc tta aaa gct gat tat 767  
 Leu Cys Val Lys Lys Ala Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr  
 155 160 165 170

gaa ttt gca gat gat tct tct ctt gac atc tct tct ggg acc act gcg 815  
 Glu Phe Ala Asp Asp Ser Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala  
 175 180 185

ctt aca gct ttt att ttt gga cg gtaagagcat ttaaattcgt atttatgaac 868  
 Leu Thr Ala Phe Ile Phe Gly Ar  
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ttctttgtag ttttgatgtg attttgaata gaattgctac tttctttctt tacag g 1044  
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agg ttg ata att gca aat gct ggt gat tgc cga gca gta ctg ggg aga 1092  
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 195 200 205 210

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 Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn Cys Thr  
 215 220 225

gcc gag aaa gta aga ata gaa aag tta ggt gga gtt gtg tat gac ggt 1188  
 Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr Asp Gly  
 230 235 240

tac ctc aac ggg caa cta tca gtt gca cgt gcc att gga gac tgg cac 1236  
 Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp Trp His  
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 260 265 270

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 275 280 285 290

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 295 300 305

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 Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly Leu Asn  
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 Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala Asn Ala Asp Val Asp  
 50 55 60  
 Val Cys Asn Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu  
 65 70 75 80  
 Pro Val Tyr Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe  
 85 90 95  
 Met Glu Asp Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly  
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 Ala Ala Ile Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly Val Phe Asp  
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 Gly His Gly Gly Thr Asp Ala Ala His Phe Val Arg Lys Asn Ile Leu  
 130 135 140

Arg Phe Ile Val Glu Asp Ser Ser Phe Pro Leu Cys Val Lys Lys Ala  
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 Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr Glu Phe Ala Asp Asp Ser  
 165 170 175  
 Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala Leu Thr Ala Phe Ile Phe  
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 Gly Arg Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu  
 195 200 205  
 Gly Arg Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn  
 210 215 220  
 Cys Thr Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr  
 225 230 235 240  
 Asp Gly Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp  
 245 250 255  
 Trp His Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu  
 260 265 270  
 Pro Glu Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile  
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 Thr Ile Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys  
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 Ser Arg Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn  
 325 330 335  
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Glu Val Pro Lys Val Ala Thr Glu Glu Ser Ser Ala Glu Val Thr Asp
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Glu Glu Thr Pro Ile Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser
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gag ccg gag cca gag gtt aaa cac gaa agt ctt ctt gaa aag ctt cac     242
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cga agc gac agt tct tct agc tcc tca agt gag gaa gaa ggt tca gat     290
Arg Ser Asp Ser Ser Ser Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp
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ggg gag aag agg aag aag aag aag gag aag aag aag cca act act gaa     338
Gly Glu Lys Arg Lys Lys Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu
                95                    100                      105

gtt gag gta aag gag gaa gag aag aaa ggg ttt atg gag aag ttg aaa     386
Val Glu Val Lys Glu Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys
                110                    115                      120

gag aag ctt cct gga cac aag aaa cct gaa gac ggt tca gcc gtc gct     434
Glu Lys Leu Pro Gly His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala
                125                    130                      135

gcg gca ccg gtg gtt gtt cct cct cct gtg gaa gaa gcg cat cca gtg     482
Ala Ala Pro Val Val Val Pro Pro Pro Val Glu Glu Ala His Pro Val
                140                    145                      150                      155

gag aag aaa ggg att ctt gag aag att aag gag aag ctt cca gga tac     530
Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr
                160                    165                      170

cac cct aag acc acc gta gag gag gag aag aaa gat aaa gaa taa       575
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 Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser Glu Pro Glu Pro Glu  
 50 55 60  
 Val Lys His Glu Ser Leu Leu Glu Lys Leu His Arg Ser Asp Ser Ser  
 65 70 75 80  
 Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp Gly Glu Lys Arg Lys  
 85 90 95  
 Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu Val Glu Val Lys Glu  
 100 105 110  
 Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys Glu Lys Leu Pro Gly  
 115 120 125  
 His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala Ala Ala Pro Val Val  
 130 135 140  
 Val Pro Pro Pro Val Glu Glu Ala His Pro Val Glu Lys Lys Gly Ile  
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 Glu Val Ala Ala Arg Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys  
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Ser	Gly	Gly	Ala	Asp	Val	Thr	Met	Tyr	Lys	Val	Thr	Glu	Arg	Thr	Thr		
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Glu	His	Pro	Pro	Glu	Gln	Asp	Arg	Pro	Gly	Val	Ile	Gly	Ser	Val	Phe		
	45					50					55						
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Arg	Ala	Val	Gln	Gly	Thr	Tyr	Glu	His	Ala	Arg	Asp	Ala	Val	Val	Gly		
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Lys	Thr	His	Glu	Ala	Ala	Glu	Ser	Thr	Lys	Glu	Gly	Ala	Gln	Ile	Ala		
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Lys	Glu	Thr	Ala	Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Val	Glu	Ala	Lys	Asp		
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Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu		
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Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Asp	Lys	Ala	Val	Glu	Ala		
	205					210					215						
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Arg	Asp	Tyr	Thr	Ala	Glu	Lys	Ala	Ile	Glu	Ala	Lys	Asp	Lys	Thr	Ala		
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Glu	Lys	Thr	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Glu	Lys	Ala	Thr	Glu		
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gaa gag acc aaa gat tct cct gcc gtg agg gga aat gaa gcg aaa ggg Glu Glu Thr Lys Asp Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly 350 355 360			1108
act att ttt ggt gca tta ggg aat gta acg gaa gca ata aag agc aaa Thr Ile Phe Gly Ala Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys 365 370 375			1156
ctg aca atg cca tca gac att gtg gag gaa aca cgc gcg gca cgt gag Leu Thr Met Pro Ser Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu 380 385 390 395			1204
cat gga ggg acg ggt agg act gtg gtt gaa gtc aag gtc gag gat tca His Gly Gly Thr Gly Arg Thr Val Val Glu Val Lys Val Glu Asp Ser 400 405 410			1252
aag ccg ggt aag gtg gcg act tca ctg aag gcg tcg gat caa atg acc Lys Pro Gly Lys Val Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr 415 420 425			1300
ggt caa aca ttc aac gac gtt gga cgg atg gat gat gat gct cgg aaa Gly Gln Thr Phe Asn Asp Val Gly Arg Met Asp Asp Ala Arg Lys 430 435 440			1348
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&lt;210&gt; 82

&lt;211&gt; 448

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 82

Met Ala Ser Asp Lys Gln Lys Ala Glu Arg Ala Glu Val Ala Ala Arg  
 1 5 10 15  
 Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys Ser Gly Gly Ala Asp  
 20 25 30  
 Val Thr Met Tyr Lys Val Thr Glu Arg Thr Thr Glu His Pro Pro Glu  
 35 40 45  
 Gln Asp Arg Pro Gly Val Ile Gly Ser Val Phe Arg Ala Val Gln Gly  
 50 55 60  
 Thr Tyr Glu His Ala Arg Asp Ala Val Val Gly Lys Thr His Glu Ala  
 65 70 75 80  
 Ala Glu Ser Thr Lys Glu Gly Ala Gln Ile Ala Ser Glu Lys Ala Val  
 85 90 95  
 Gly Ala Lys Asp Ala Thr Val Glu Lys Ala Lys Glu Thr Ala Asp Tyr  
 100 105 110  
 Thr Ala Glu Lys Val Gly Glu Tyr Lys Asp Tyr Thr Val Asp Lys Ala  
 115 120 125  
 Lys Glu Ala Lys Asp Thr Thr Ala Glu Lys Ala Lys Glu Thr Ala Asn  
 130 135 140  
 Tyr Thr Ala Asp Lys Ala Val Glu Ala Lys Asp Lys Thr Ala Glu Lys  
 145 150 155 160  
 Ile Gly Glu Tyr Lys Asp Tyr Ala Val Asp Lys Ala Val Glu Ala Lys  
 165 170 175  
 Asp Lys Thr Ala Glu Lys Ala Lys Glu Thr Ser Asn Tyr Thr Ala Asp  
 180 185 190  
 Lys Ala Lys Glu Ala Lys Asp Lys Thr Ala Glu Lys Val Gly Glu Tyr  
 195 200 205  
 Lys Asp Tyr Thr Val Asp Lys Ala Val Glu Ala Arg Asp Tyr Thr Ala  
 210 215 220  
 Glu Lys Ala Ile Glu Ala Lys Asp Lys Thr Ala Glu Lys Thr Gly Glu  
 225 230 235 240  
 Tyr Lys Asp Tyr Thr Val Glu Lys Ala Thr Glu Gly Lys Asp Val Thr  
 245 250 255  
 Val Ser Lys Leu Gly Glu Leu Lys Asp Ser Ala Val Glu Thr Ala Lys  
 260 265 270  
 Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu Glu Ala Lys Gly Lys  
 275 280 285  
 Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn Met Glu Lys Ala Gly  
 290 295 300

Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg Leu Glu Gly Lys Glu  
 305 310 315 320  
 Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu Ala Ser Gln Lys Thr  
 325 330 335  
 Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala Glu Glu Thr Lys Asp  
 340 345 350  
 Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly Thr Ile Phe Gly Ala  
 355 360 365  
 Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys Leu Thr Met Pro Ser  
 370 375 380  
 Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu His Gly Gly Thr Gly  
 385 390 395 400  
 Arg Thr Val Val Glu Val Lys Val Glu Asp Ser Lys Pro Gly Lys Val  
 405 410 415  
 Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr Gly Gln Thr Phe Asn  
 420 425 430  
 Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys Asp Lys Gly Lys Leu  
 435 440 445

<210> 83  
 <211> 561  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (18) .. (548)

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 Met Asn Glu Met Ser Phe Phe Gly Tyr Ser Phe  
 1 5 10  
 atc gta gta gca tta ttc ttc gat tta act caa gcc tat cgt cac act 98  
 Ile Val Val Ala Leu Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr  
 15 20 25  
 ccc gct caa ccg cca aaa gca aac gca aac ggt gat gtc aaa ccg caa 146  
 Pro Ala Gln Pro Pro Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln  
 30 35 40  
 gaa acg ctc gtg gtt cac aac aag gcc cga gcc atg gtc gga gtc gga 194  
 Glu Thr Leu Val Val His Asn Lys Ala Arg Ala Met Val Gly Val Gly  
 45 50 55  
 cca atg gtg tgg aac gaa act ctt gcg acc tat gca cag agc tac gca 242  
 Pro Met Val Trp Asn Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala

60	65	70	75	
cat gaa cga gcc aga gac tgt gcc atg aag cat tcc ttg gga cca ttc				290
His Glu Arg Ala Arg Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe	80	85	90	
ggc gag aat cta gcc gcg ggt tgg gga acg atg agc ggt ccg gta gca				338
Gly Glu Asn Leu Ala Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala	95	100	105	
act gag tat tgg atg acg gag aag gaa aat tac gat tat gat agt aac				386
Thr Glu Tyr Trp Met Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn	110	115	120	
acg tgt ggt ggt gat ggt gtg tgt gga cac tac act cag atc gtg tgg				434
Thr Cys Gly Gly Asp Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp	125	130	135	
cgt gac tcg gtt cga ctt ggt tgt gcc tcc gtg aga tgt aag aat gat				482
Arg Asp Ser Val Arg Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp	140	145	150	155
gag tat att tgg gtg att tgt agc tat gat cct ccg ggg aat tac atc				530
Glu Tyr Ile Trp Val Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile	160	165	170	
ggt caa cgt cca tat tag tgattggatt tta				561
Gly Gln Arg Pro Tyr	175			

&lt;210&gt; 84

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 84

Met Asn Glu Met Ser Phe Phe Gly Tyr Ser Phe Ile Val Val Ala Leu	1	5	10	15
Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr Pro Ala Gln Pro Pro	20	25	30	
Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln Glu Thr Leu Val Val	35	40	45	
His Asn Lys Ala Arg Ala Met Val Gly Val Gly Pro Met Val Trp Asn	50	55	60	
Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala His Glu Arg Ala Arg	65	70	75	80
Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe Gly Glu Asn Leu Ala	85	90	95	
Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala Thr Glu Tyr Trp Met	100	105	110	

Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn Thr Cys Gly Gly Asp  
 115 120 125

Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp Arg Asp Ser Val Arg  
 130 135 140

Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp Glu Tyr Ile Trp Val  
 145 150 155 160

Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile Gly Gln Arg Pro Tyr  
 165 170 175

<210> 85  
 <211> 988  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
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 Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe  
 1 5 10

tta gtt ttg ttg ttt gct caa gcc aat tcg caa ggt ttg aaa gta ggt 98  
 Leu Val Leu Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly  
 15 20 25

ttc tac agc aaa aca tgc cca caa ctc gag ggt ata gtt aaa aag gtc 146  
 Phe Tyr Ser Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val  
 30 35 40 45

gtg ttc gat gcg atg aac aaa gca cca aca ctt ggt gct cct ttg ctt 194  
 Val Phe Asp Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu  
 50 55 60

aga atg ttc ttc cac gac tgc ttc gtt cgg gga tgt gac gga tca gtt 242  
 Arg Met Phe Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val  
 65 70 75

ttg tta gat aaa cca aac aat caa ggt gag aag agt gca gtt cct aac 290  
 Leu Leu Asp Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn  
 80 85 90

cta agt ctt cga ggg ttt ggc atc ata gac gat tcc aag gcg gct cta 338  
 Leu Ser Leu Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu  
 95 100 105

gaa aaa gtg tgt ccg gga att gtt tct tgc tct gat atc ttg gca ctt 386  
 Glu Lys Val Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu  
 110 115 120 125

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gtc gct aga gac gca atg gtt gca ctt gaa gga cca tca tgg gaa gtt 434
Val Ala Arg Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val
      130      135      140

gaa acg gga aga aga gac ggt agg gtt tct aac atc aac gaa gtc aac 482
Glu Thr Gly Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn
      145      150      155

ttg cca tca cct ttt gat aac atc acc aag ctt atc agc gat ttt cgc 530
Leu Pro Ser Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg
      160      165      170

tca aag ggc ctc aac gag aag gat cta gtc att ctc tcg ggt ggt cac 578
Ser Lys Gly Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His
      175      180      185

aca att gga atg gga cat tgt cct tta ttg aca aac cgg ctt tac aac 626
Thr Ile Gly Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn
      190      195      200      205

ttc acc gga aaa gga gac agc gac cca agt ttg gac tcg gag tac gcc 674
Phe Thr Gly Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala
      210      215      220

gct aag ctc agg aag aaa tgc aag ccc acc gat acg acg acg gct cta 722
Ala Lys Leu Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu
      225      230      235

gag atg gat ccg ggg agt ttc aaa aca ttt gac ttg agc tac ttc acg 770
Glu Met Asp Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr
      240      245      250

cta gtg gct aag aga aga gga ctt ttc cag tcg gat gct gct cta ctc 818
Leu Val Ala Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu
      255      260      265

gac aac tcc aag act agg gct tat gtc ttg caa cag ata aga act cat 866
Asp Asn Ser Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His
      270      275      280      285

ggg tca atg ttc ttt aac gac ttt ggt gtc tct atg gtg aaa atg ggt 914
Gly Ser Met Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly
      290      295      300

cgg act gga gtt ctt acg ggt aag gcc ggg gag atc cgt aag acg tgt 962
Arg Thr Gly Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys
      305      310      315

cgg tct gct aat taa gagatataga aa 989
Arg Ser Ala Asn
      320

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&lt;210&gt; 86

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 86

Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe Leu Val Leu  
 1 5 10 15  
 Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly Phe Tyr Ser  
 20 25 30  
 Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val Val Phe Asp  
 35 40 45  
 Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu Arg Met Phe  
 50 55 60  
 Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Leu Asp  
 65 70 75 80  
 Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn Leu Ser Leu  
 85 90 95  
 Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu Glu Lys Val  
 100 105 110  
 Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu Val Ala Arg  
 115 120 125  
 Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val Glu Thr Gly  
 130 135 140  
 Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn Leu Pro Ser  
 145 150 155 160  
 Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg Ser Lys Gly  
 165 170 175  
 Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His Thr Ile Gly  
 180 185 190  
 Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn Phe Thr Gly  
 195 200 205  
 Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala Ala Lys Leu  
 210 215 220  
 Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu Glu Met Asp  
 225 230 235 240  
 Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr Leu Val Ala  
 245 250 255  
 Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu Asp Asn Ser  
 260 265 270  
 Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His Gly Ser Met  
 275 280 285  
 Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly Arg Thr Gly

290	295	300	
Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys Arg Ser Ala			
305	310	315	320
Asn			
<210> 87			
<211> 650			
<212> DNA			
<213> Arabidopsis thaliana			
<220>			
<221> CDS			
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Met Ala Ser Ile Thr Asn Leu Ala Ser Ser Leu Ser Ser Leu			
1	5	10	
tcg ttc tcc tcc caa gtt tct caa aga cct aac acc att tcc ttc ccc			97
Ser Phe Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro			
15	20	25	30
cgc gcg aat tca gta ttc gca tta ccg gcg aaa tcc gca cgc cgc gct			145
Arg Ala Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala			
35	40	45	
tct cta tct atc acc gcc acg gta tct gct cca ccg gag gag gag gag			193
Ser Leu Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu			
50	55	60	
ata gtt gaa ctg aag aaa tac gtc aaa tcg agg ctt ccc gga gga ttt			241
Ile Val Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe			
65	70	75	
gct gct cag aag att att ggc act gga cga cgt aag tgc gca atc gct			289
Ala Ala Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala			
80	85	90	
aga gtt gtt ctt cag gaa ggt act ggg aag gtt atc atc aac tat cgt			337
Arg Val Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg			
95	100	105	110
gat gcc aag gag tac ctt cag gga aat cca ttg tgg ctt cag tat gtt			385
Asp Ala Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val			
115	120	125	
aaa gta cca ttg gtg act tta gga tat gag aat agc tac gac ata ttt			433
Lys Val Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe			
130	135	140	
gtg aaa gcc cat gga ggc ggt ctc tca ggt caa gct caa gca att acc			481
Val Lys Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr			

145	150	155	
ttg gga gtc gca cgt gca ctc ctg aag gta agt gca gac cac aga tcg			529
Leu Gly Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser			
160	165	170	
cct ttg aag aag gaa ggt ttg ctc act aga gat gcg aga gtg gtt gaa			577
Pro Leu Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu			
175	180	185	190
aga aag aag gcc ggg ctc aag aag gcg cgt aaa gcc cca caa ttc tcc			625
Arg Lys Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser			
195	200	205	
aag cgt taa gagttttata tatcat			650
Lys Arg			

<210> 88  
 <211> 208  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 88
Met Ala Ser Ile Thr Asn Leu Ala Ser Ser Leu Ser Ser Leu Ser Phe
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20 25 30
Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala Ser Leu
35 40 45
Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu Ile Val
50 55 60
Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe Ala Ala
65 70 75 80
Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala Arg Val
85 90 95
Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg Asp Ala
100 105 110
Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val Lys Val
115 120 125
Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe Val Lys
130 135 140
Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr Leu Gly
145 150 155 160
Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser Pro Leu
165 170 175

Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu Arg Lys  
 180 185 190

Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser Lys Arg  
 195 200 205

<210> 89

<211> 1223

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (16)..(1215)

<400> 89

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          1              5              10

gagatggctcggactcagaaagaataaagctacagagtattcatcttggt99
Glu Met Ala Arg Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly
      15              20              25

cagctcaaggaagaattgcaaaactcaggacacaaatgttgagagcc147
Gln Leu Lys Ala Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro
      30              35              40

cca aaa ggt gct agt gga ggc ggg gaa ggt ttt gaa gtt acc aag tat 195
Pro Lys Gly Ala Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr
      45              50              55              60

gggcatggaagtggtgcacttataggatttctcagtgctggaagagttcc243
Gly His Gly Arg Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser
      65              70              75

acgcttttgactatgttatggaacacatcttgaaagcagccatcatat291
Thr Leu Leu Thr Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr
      80              85              90

gaattttacacacttacaatgcattcctgggtgtaattcacatcaaacgac339
Glu Phe Thr Thr Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp
      95              100              105

aca aag att cag ctt ctc gat ctt cct ggg att att gaa ggt gct tcg 387
Thr Lys Ile Gln Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser
      110              115              120

gaa gga aag ggg cga gga agg cag gtt att gct gtt gca aag tct tcc 435
Glu Gly Lys Gly Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser
      125              130              135              140

gac ctt gta ttg atg gtt ctt gat gcc tca aaa agc gaa ggc cac agg 483
Asp Leu Val Leu Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg
      145              150              155

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caa ata ttg act aag gaa ctt gag gca gtg ggc ttg cga cta aac aaa	531
Gln Ile Leu Thr Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys	
160 165 170	
act cct ccg cag ata tac ttt aaa aag aaa aag act ggt gga atc tct	579
Thr Pro Pro Gln Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser	
175 180 185	
ttc aac act aca gca ccc ttg act cac att gat gag aag ctc tgt tat	627
Phe Asn Thr Thr Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr	
190 195 200	
caa atc ctg cat gaa tac aag att cac aat gct gag gtg cta ttt cgt	675
Gln Ile Leu His Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg	
205 210 215 220	
gag aat gcc aca gtg gat gac ttt att gat gtc att gaa ggc aac cgc	723
Glu Asn Ala Thr Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg	
225 230 235	
aag tat att aag tgt gtt tat gtc tac atc aaa ata gat gtt gtt gga	771
Lys Tyr Ile Lys Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly	
240 245 250	
att gat gat gtg gat aga cta tcc cgg cag cca aat tcc att gtt att	819
Ile Asp Asp Val Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile	
255 260 265	
agc tgc aat ctt aag ctt aac tta gac aga cta ctt gct agg atg tgg	867
Ser Cys Asn Leu Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp	
270 275 280	
gac gaa atg ggc ctt gtg aga gtt tac tcg aag ccg caa ggc cag caa	915
Asp Glu Met Gly Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln	
285 290 295 300	
cca gat ttc gat gag cct ttt gtc ctc tca tct gat cga ggt ggc tgc	963
Pro Asp Phe Asp Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys	
305 310 315	
aca gtg gaa gac ttc tgt aac cac gtc cac agg act ctg gtg aag gat	1011
Thr Val Glu Asp Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp	
320 325 330	
atg aag tat gca ctc gtt tgg ggc aca agc aca agg cac aat cca cag	1059
Met Lys Tyr Ala Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln	
335 340 345	
aat tgt ggt ctt tct caa cat ctt gaa gac gaa gat gtt gtt cag atc	1107
Asn Cys Gly Leu Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile	
350 355 360	
gtc aag aaa aag gag aga gac gaa gga gga aga ggc cgg ttc aag tca	1155
Val Lys Lys Lys Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser	
365 370 375 380	

cac tca aac gcc cct gct aga att gca gac aga gag aaa aaa gct cct 1203  
 His Ser Asn Ala Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro  
                   385                                  390                                  395

ctt aag caa taa gcttttag 1223  
 Leu Lys Gln  
                   400

<210> 90  
 <211> 399  
 <212> PRT  
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                   20                                  25                                  30  
 Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro Pro Lys Gly Ala  
                   35                                  40                                  45  
 Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr Gly His Gly Arg  
                   50                                  55                                  60  
 Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Thr  
                   65                                  70                                  75                                  80  
 Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr Glu Phe Thr Thr  
                   85                                  90                                  95  
 Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp Thr Lys Ile Gln  
                   100                                  105                                  110  
 Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser Glu Gly Lys Gly  
                   115                                  120                                  125  
 Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser Asp Leu Val Leu  
                   130                                  135                                  140  
 Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg Gln Ile Leu Thr  
                   145                                  150                                  155                                  160  
 Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys Thr Pro Pro Gln  
                   165                                  170                                  175  
 Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser Phe Asn Thr Thr  
                   180                                  185                                  190  
 Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr Gln Ile Leu His  
                   195                                  200                                  205  
 Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg Glu Asn Ala Thr  
                   210                                  215                                  220

Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg Lys Tyr Ile Lys  
 225 230 235 240  
 Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly Ile Asp Asp Val  
 245 250 255  
 Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile Ser Cys Asn Leu  
 260 265 270  
 Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp Asp Glu Met Gly  
 275 280 285  
 Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln Pro Asp Phe Asp  
 290 295 300  
 Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys Thr Val Glu Asp  
 305 310 315 320  
 Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp Met Lys Tyr Ala  
 325 330 335  
 Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln Asn Cys Gly Leu  
 340 345 350  
 Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile Val Lys Lys Lys  
 355 360 365  
 Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser His Ser Asn Ala  
 370 375 380  
 Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro Leu Lys Gln  
 385 390 395

<210> 91  
 <211> 536  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (12)..(524)

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 Met Thr Ser Ser Asp Gln Ser Pro Ser His Asp Val Phe  
 1 5 10  
 gtc tac ggc agt ttc caa gaa cca gcc gtt gtt aat tta att ctc gaa 98  
 Val Tyr Gly Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu  
 15 20 25  
 tgt gct ccg gtc atg gtt tcc gct caa ctc cac ggc tat cac ttg tat 146  
 Cys Ala Pro Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr  
 30 35 40 45

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aga ctt aaa ggt cgt ttg cat cca tgt att tct cct tcc gac aat gga 194
Arg Leu Lys Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly
      50                      55                      60

tta atc aat ggc aag ata cta act gga tta aca gat tct cag tta gag 242
Leu Ile Asn Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu
      65                      70                      75

agt tta gat atg att gaa gga act gaa tat gtg agg aag act gtt gaa 290
Ser Leu Asp Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu
      80                      85                      90

gtt gtt ttg act gat act ttg gag aag aag caa gtt gaa aca att gta 338
Val Val Leu Thr Asp Thr Leu Glu Lys Lys Gln Val Glu Thr Ile Val
      95                      100                     105

tgg gca aac aag gat gat cct aat atg tat gga gaa tgg gat ttc gag 386
Trp Ala Asn Lys Asp Asp Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu
     110                      115                     120                     125

gaa tgg aag agg ctt cat atg gag aaa ttt ata gag gcg gcg acg aaa 434
Glu Trp Lys Arg Leu His Met Glu Lys Phe Ile Glu Ala Ala Thr Lys
      130                      135                     140

ttc atg gag tgg aag aag aat ccg aat ggg aga agt agg gaa gag ttt 482
Phe Met Glu Trp Lys Lys Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe
      145                      150                     155

gag aag ttt gta caa gat gat tct tct ccg gct tcg gct tga 524
Glu Lys Phe Val Gln Asp Asp Ser Ser Pro Ala Ser Ala
      160                      165                     170

agaagttgtt ta 536

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<210> 92  
 <211> 170  
 <212> PRT  
 <213> Arabidopsis thaliana

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Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu Cys Ala Pro
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Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr Arg Leu Lys
      35           40           45

Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly Leu Ile Asn
      50           55           60

Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu Ser Leu Asp
      65           70           75           80

Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu Val Val Leu

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				85						90				95	
Thr	Asp	Thr	Leu	Glu	Lys	Lys	Gln	Val	Glu	Thr	Ile	Val	Trp	Ala	Asn
			100					105					110		
Lys	Asp	Asp	Pro	Asn	Met	Tyr	Gly	Glu	Trp	Asp	Phe	Glu	Glu	Trp	Lys
		115					120					125			
Arg	Leu	His	Met	Glu	Lys	Phe	Ile	Glu	Ala	Ala	Thr	Lys	Phe	Met	Glu
	130					135					140				
Trp	Lys	Lys	Asn	Pro	Asn	Gly	Arg	Ser	Arg	Glu	Glu	Phe	Glu	Lys	Phe
145					150					155					160
Val	Gln	Asp	Asp	Ser	Ser	Pro	Ala	Ser	Ala						
				165					170						

<210> 93  
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 <222> (16)..(71)

<220>  
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 <222> (197)..(278)

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 aaa tgt ggt gat tcg tgc ag gtaaacccta gattctctct tcattaactt 101  
 Lys Cys Gly Asp Ser Cys Se  
                   15  
 atcatgcata tatatcctaa tatacatgtg gttacatatt ccttaagata aattttgaaa 161  
 tcttataactt ctgttgtttt ttgggtatga caaag t tgc gag aag aac tac aac 215  
   r Cys Glu Lys Asn Tyr Asn  
   20                  25  
 aag gag tgt gat aac tgt agc tgt gga tca aac tgc agc tgc ggg tca 263  
 Lys Glu Cys Asp Asn Cys Ser Cys Gly Ser Asn Cys Ser Cys Gly Ser  
                   30                  35                  40  
 agc tgt aac tgt tga agaaattatc agcat 293  
 Ser Cys Asn Cys  
                   45

<210> 94

<211> 45  
 <212> PRT  
 <213> Arabidopsis thaliana

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 Ser Cys Ser Cys Glu Lys Asn Tyr Asn Lys Glu Cys Asp Asn Cys Ser  
                   20                  25                  30  
 Cys Gly Ser Asn Cys Ser Cys Gly Ser Ser Cys Asn Cys  
                   35                  40                  45

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 <222> (14)..(868)

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                   1                  5                  10  
 Met Ser Ala Ser Ser Leu Phe Asn Leu Pro Leu Ile  
 cgc ctc aga tct ctc gct ctt tcg tct tct ttt tct tct ttc cga ttt 97  
 Arg Leu Arg Ser Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe  
                   15                  20                  25  
 gcc cat cgt cct ctg tca tcg att tca ccg aga aag tta ccg aat ttt 145  
 Ala His Arg Pro Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe  
                   30                  35                  40  
 cgt gct ttc tct ggt acc gct atg aca gat act aaa gat gct ggt atg 193  
 Arg Ala Phe Ser Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met  
                   45                  50                  55                  60  
 gat gct gtt cag aga cgt ctc atg ttt gag gat gaa tgc att ctt gtt 241  
 Asp Ala Val Gln Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val  
                   65                  70                  75  
 gat gaa act gat cgt gtt gtg ggg cat gac agc aag tat aat tgt cat 289  
 Asp Glu Thr Asp Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His  
                   80                  85                  90  
 ctg atg gaa aat att gaa gcc aag aat ttg ctg cac agg gct ttt agt 337  
 Leu Met Glu Asn Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser  
                   95                  100                  105  
 gta ttt tta ttc aac tcg aag tat gag ttg ctt ctc cag caa agg tca 385  
 Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu Gln Gln Arg Ser  
                   110                  115                  120

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aac aca aag gtt acg ttc cct cta gtg tgg act aac act tgt tgc agc 433
Asn Thr Lys Val Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser
125 130 135 140

cat cct ctt tac cgt gaa tca gag ctt atc cag gac aat gca cta ggt 481
His Pro Leu Tyr Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly
145 150 155

gtg agg aat gct gca caa aga aag ctt ctc gat gag ctt ggt att gta 529
Val Arg Asn Ala Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val
160 165 170

gct gaa gat gta cca gtc gat gag ttc act ccc ttg gga cgt atg ctg 577
Ala Glu Asp Val Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu
175 180 185

tac aag gct cct tct gat ggc aaa tgg gga gag cat gaa ctt gat tac 625
Tyr Lys Ala Pro Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr
190 195 200

ttg ctc ttc atc gtg cga gac gtg aag gtt caa cca aac cca gat gaa 673
Leu Leu Phe Ile Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu
205 210 215 220

gta gct gag atc aag tat gtg agc cgg gaa gag ctg aag gag ctg gtg 721
Val Ala Glu Ile Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val
225 230 235

aag aaa gca gat gca ggt gag gaa ggt ttg aaa ctg tca cca tgg ttc 769
Lys Lys Ala Asp Ala Gly Glu Glu Lys Leu Lys Leu Ser Pro Trp Phe
240 245 250

aga ttg gtg gtg gac aat ttc ttg atg aag tgg tgg gat cat gta gag 817
Arg Leu Val Val Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu
255 260 265

aaa gga act ttg gtt gaa gct ata gac atg aaa acc atc cac aaa ctc 865
Lys Gly Thr Leu Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu
270 275 280

tga acatcttttt tt 880

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285

&lt;210&gt; 96

&lt;211&gt; 284

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 96

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Met Ser Ala Ser Ser Leu Phe Asn Leu Pro Leu Ile Arg Leu Arg Ser
1 5 10 15

```

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Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe Ala His Arg Pro
20 25 30

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Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe Arg Ala Phe Ser  
           35                          40                          45  
 Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met Asp Ala Val Gln  
           50                          55                          60  
 Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val Asp Glu Thr Asp  
           65                          70                          75                          80  
 Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Asn  
                           85                          90                          95  
 Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe  
                           100                          105                          110  
 Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser Asn Thr Lys Val  
           115                          120                          125  
 Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr  
           130                          135                          140  
 Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly Val Arg Asn Ala  
           145                          150                          155                          160  
 Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val Ala Glu Asp Val  
                           165                          170                          175  
 Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro  
           180                          185                          190  
 Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile  
           195                          200                          205  
 Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu Val Ala Glu Ile  
           210                          215                          220  
 Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val Lys Lys Ala Asp  
           225                          230                          235                          240  
 Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val  
                           245                          250                          255  
 Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu Lys Gly Thr Leu  
           260                          265                          270  
 Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu  
           275                          280

&lt;210&gt; 97

&lt;211&gt; 831

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (18)..(821)

&lt;400&gt; 97

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tgcaactac aacctca atg gcc gcc tca aca atg gct ctc tcc tcc cct    50
      Met Ala Ala Ser Thr Met Ala Leu Ser Ser Pro
        1              5              10

gcc ttc gcc ggt aag gcc gtc aag ctt tcc ccc gcg gca tca gaa gtc    98
Ala Phe Ala Gly Lys Ala Val Lys Leu Ser Pro Ala Ala Ser Glu Val
      15              20              25

ctt gga agc ggc cgt gtg aca atg agg aag act gtt gcc aag cca aag   146
Leu Gly Ser Gly Arg Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys
      30              35              40

ggc cca tca ggc agc cca tgg tac gga tct gac cgt gtc aag tac ttg   194
Gly Pro Ser Gly Ser Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu
      45              50              55

ggt cca ttc tct ggc gaa tca ccg agc tac ctt acc gga gag ttc ccc   242
Gly Pro Phe Ser Gly Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro
      60              65              70              75

gga gac tac gga tgg gac acc gcc gga ctt tca gct gac ccc gag aca   290
Gly Asp Tyr Gly Trp Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr
      80              85              90

ttc gca agg aac cgt gaa cta gaa gtt atc cac agc agg tgg gct atg   338
Phe Ala Arg Asn Arg Glu Leu Glu Val Ile His Ser Arg Trp Ala Met
      95              100             105

ctc gga gcc cta ggc tgc gtc ttc cct gag ctt ttg gct aga aac gga   386
Leu Gly Ala Leu Gly Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly
     110              115             120

gtc aag ttc gga gag gcg gtt tgg ttc aag gcc ggt tca cag atc ttc   434
Val Lys Phe Gly Glu Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe
     125              130             135

agc gat gga ggg ctc gat tac ttg gga aac cct agc ttg gtt cac gct   482
Ser Asp Gly Gly Leu Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala
    140              145             150             155

cag agc att ttg gcc att tgg gcc aca caa gtt att ttg atg gga gcc   530
Gln Ser Ile Leu Ala Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala
     160              165             170

gtt gaa ggc tac aga gtc gca gga aat ggg cca ttg gga gag gcc gag   578
Val Glu Gly Tyr Arg Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu
     175              180             185

gac ttg ctt tac ccc ggt ggc agc ttc gac cca ttg ggt ttg gct acc   626
Asp Leu Leu Tyr Pro Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr
     190              195             200

gac cca gag gca ttc gct gag ttg aag gtg aag gag ctc aag aac gga   674

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Asp Pro Glu Ala Phe Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly  
 205 210 215  
 aga ttg gct atg ttc tct atg ttt gga ttc ttc gtt caa gcc atc gtc 722  
 Arg Leu Ala Met Phe Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val  
 220 225 230 235  
 act ggt aag gga ccg ata gag aac ctt gct gac cat ttg gcc gat cca 770  
 Thr Gly Lys Gly Pro Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro  
 240 245 250  
 gtt aac aac aac gca tgg gcc ttc gcc acc aac ttt gtt ccc gga aag 818  
 Val Asn Asn Asn Ala Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys  
 255 260 265  
 tga gccaaagtttt 831

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 <211> 267  
 <212> PRT  
 <213> Arabidopsis thaliana

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 20 25 30  
 Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys Gly Pro Ser Gly Ser  
 35 40 45  
 Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu Gly Pro Phe Ser Gly  
 50 55 60  
 Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro Gly Asp Tyr Gly Trp  
 65 70 75 80  
 Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Arg Asn Arg  
 85 90 95  
 Glu Leu Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly  
 100 105 110  
 Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly Val Lys Phe Gly Glu  
 115 120 125  
 Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Asp Gly Gly Leu  
 130 135 140  
 Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala Gln Ser Ile Leu Ala  
 145 150 155 160  
 Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala Val Glu Gly Tyr Arg  
 165 170 175

Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu Asp Leu Leu Tyr Pro  
 180 185 190

Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr Asp Pro Glu Ala Phe  
 195 200 205

Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly Arg Leu Ala Met Phe  
 210 215 220

Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val Thr Gly Lys Gly Pro  
 225 230 235 240

Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro Val Asn Asn Asn Ala  
 245 250 255

Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys  
 260 265

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 <222> (15)..(164)

<220>  
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 <222> (257)..(305)

<220>  
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 <222> (416)..(843)

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 1 5 10

aca gcc act aga aga gtt ctc atc gct ctt cac gag aag aat gtc gac 98  
 Thr Ala Thr Arg Arg Val Leu Ile Ala Leu His Glu Lys Asn Val Asp  
 15 20 25

ttt gaa ttc gtt cat gtc gag ctc aaa gat ggt gaa cac aag aaa gag 146  
 Phe Glu Phe Val His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu  
 30 35 40

cct ttc atc ctt cgc aac gtgagtacat ataacatctg tcaagccaaa 194  
 Pro Phe Ile Leu Arg Asn  
 45 50

atattgtatt tcacttagat actgaatctt ggtcttaaca atcttgaata atgtttttgc 254

ag ccc ttt ggt aaa gtt cca gcc ttt gaa gat gga gac ttc aag att 301  
 Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys Ile  
 55 60 65  
 ttc g gtaaatacaa atatatatca ttatagtcac gtttacaaat ttttggtttt 355  
 Phe G  
 atgatcattg caataataga aagcagaaac actcaaaaat gttttttttt tgggtgggcag 415  
 aa tca aga gca att act caa tac ata gct cat gaa ttc tca gac aaa 462  
 lu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser Asp Lys  
 70 75 80  
 gga aac aac ctt ctc tca act ggc aag gac atg gcg atc ata gcc atg 510  
 Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile Ala Met  
 85 90 95  
 ggc att gaa att gag tcg cat gag ttt gac cca gtt ggt tca aag ctt 558  
 Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser Lys Leu  
 100 105 110  
 gtt tgg gag caa gtc tta aag cct ttg tat ggt atg acc aca gac aaa 606  
 Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr Asp Lys  
 115 120 125  
 act gtt gtt gaa gaa gaa gag gct aag cta gcc aaa gtc ctc gat gtt 654  
 Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu Asp Val  
 130 135 140 145  
 tac gaa cac agg ctt ggt gag tcc aag tat ttg gct tct gac cac ttc 702  
 Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp His Phe  
 150 155 160  
 act ttg gtc gat ctt cac act atc cct gtg att caa tac tta ctt gga 750  
 Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu Leu Gly  
 165 170 175  
 act cca act aag aaa ctc ttc gac gag cgt cca cat gtg agt gct tgg 798  
 Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser Ala Trp  
 180 185 190  
 gtt gct gac atc act tca agg cct tct gct cag aag gtt ctt taa 843  
 Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu  
 195 200 205  
 gtgaatctca aa 855

&lt;210&gt; 100

&lt;211&gt; 208

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 100

Met Ala Gly Ile Lys Val Phe Gly His Pro Ala Ser Thr Ala Thr Arg  
 1 5 10 15

Arg Val Leu Ile Ala Leu His Glu Lys Asn Val Asp Phe Glu Phe Val  
                   20                                  25                                  30  
 His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu Pro Phe Ile Leu  
                   35                                  40                                  45  
 Arg Asn Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys  
                   50                                  55                                  60  
 Ile Phe Glu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser  
                   65                                  70                                  75                                  80  
 Asp Lys Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile  
                                   85                                  90                                  95  
 Ala Met Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser  
                                   100                                  105                                  110  
 Lys Leu Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr  
                                   115                                  120                                  125  
 Asp Lys Thr Val Val Glu Glu Glu Ala Lys Leu Ala Lys Val Leu  
                   130                                  135                                  140  
 Asp Val Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp  
                   145                                  150                                  155                                  160  
 His Phe Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu  
                                   165                                  170                                  175  
 Leu Gly Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser  
                                   180                                  185                                  190  
 Ala Trp Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu  
                   195                                  200                                  205

&lt;210&gt; 101

&lt;211&gt; 512

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (12)..(67)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (241)..(309)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (417)..(492)

&lt;400&gt; 101

tatctgaaaa a atg tca gag acc aac aag aat gcc ttc caa gcc ggt cag 50

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      Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln
      1           5           10
acc gct ggc aaa gct ga ggtactactc tttctctctt tgacagaact      97
Thr Ala Gly Lys Ala Gl
      15

cttaaactgg aaaaattggt gaagctataa ctctttgaaa acagttgaaa cttgatcatt 157
actagaaatt tcagttactt gtttaattta gtttgcgta attatgtaat tgatgatttt 217
atgggtacaa tggttgtcat gta g gag aag agc aat gtt ctg ctg gac aag      268
                        u Glu Lys Ser Asn Val Leu Leu Asp Lys
                        20           25

gcc aag gat gct gca gct ggt gct gga gct gga gca caa ca ggtaaacaat 319
Ala Lys Asp Ala Ala Ala Gly Ala Gly Ala Gly Ala Gln Gl
      30           35           40

ccatacacag acacataaca tataatatgt aacgaaataa acgtctttgt aagcttacat 379
gtacgcagat ttctgatatg gttatgtata tgttata g gcg gga aag agt gta      432
                        n Ala Gly Lys Ser Val
                        45

tcg gat gcg gca gcg gga ggt gtt aac ttc gtg aag gac aag acc ggc      480
Ser Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly
      50           55           60

ctg aac aag tag agattcgggt caaatttggg      512
Leu Asn Lys
      65

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<210> 102  
 <211> 66  
 <212> PRT  
 <213> Arabidopsis thaliana

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<400> 102
Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln Thr Ala Gly
  1           5           10           15

Lys Ala Glu Glu Lys Ser Asn Val Leu Leu Asp Lys Ala Lys Asp Ala
      20           25           30

Ala Ala Gly Ala Gly Ala Gly Ala Gln Gln Ala Gly Lys Ser Val Ser
      35           40           45

Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly Leu
      50           55           60

Asn Lys
      65

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<210> 103  
 <211> 1138  
 <212> DNA  
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<220>  
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 <222> (11)..(1123)

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                   1                  5                  10  
                   Met Ala Thr Leu Val Asp Pro Pro Asn Gly Ile Arg Asn  
 gaa ggg aag cat tac ttc tca atg tgg caa act ctg ttc gag atc gac 97  
 Glu Gly Lys His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp  
           15                  20                  25  
 act aag tac atg cct atc aag cct att ggt cgt gga gct tac ggt gtt 145  
 Thr Lys Tyr Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val  
           30                  35                  40                  45  
 gtc tgc tcc tct gtt aac agt gac acc aac gag aaa gtt gct atc aag 193  
 Val Cys Ser Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys  
                   50                  55                  60  
 aag att cac aat gtt tat gag aat agg atc gat gcg ttg agg act ctt 241  
 Lys Ile His Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu  
                   65                  70                  75  
 cgg gag ctc aag ctt cta cgc cat ctt cga cat gag aat gtc att gct 289  
 Arg Glu Leu Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala  
                   80                  85                  90  
 ttg aaa gat gtc atg atg cca att cat aag atg agc ttc aag gat gtt 337  
 Leu Lys Asp Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val  
           95                  100                  105  
 tat ctt gtt tat gag ctc atg gac act gat ctc cac cag att atc aag 385  
 Tyr Leu Val Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys  
           110                  115                  120                  125  
 tct tct cag cgt ctt agt aac gat cat tgc caa tac ttc ttg ttc cag 433  
 Ser Ser Gln Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln  
                   130                  135                  140  
 ttg ctt cga ggg ctc aag tat att cat tca gcc aat atc ctg cac cga 481  
 Leu Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg  
                   145                  150                  155  
 gat ttg aaa cct ggt aac ctt ctt gtc aac gca aac tgc gat tta aag 529  
 Asp Leu Lys Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys  
                   160                  165                  170  
 ata tgc gat ttt gga cta gcg cgt gcg agc aac acc aag ggt cag ttc 577  
 Ile Cys Asp Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe  
           175                  180                  185

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atg act gaa tat gtt gtg act cgt tgg tac cga gcc cca gag ctt ctc 625
Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu
190                195                200                205

ctc tgt tgt gac aac tat gga aca tcc att gat gtt tgg tct gtt ggt 673
Leu Cys Cys Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly
                210                215                220

tgc att ttc gcc gag ctt ctt ggt agg aaa ccg ata ttc caa gga acg 721
Cys Ile Phe Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr
                225                230                235

gaa tgt ctt aac cag ctt aag ctc att gtc aac att atc gga agc caa 769
Glu Cys Leu Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln
                240                245                250

aga gaa gaa gat ctt gag ttc ata gtt aac ccg aaa gct aaa aga tac 817
Arg Glu Glu Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr
                255                260                265

att aga tca ctt ccg tac tca cct ggg atg tct tta tcc aga ctt tac 865
Ile Arg Ser Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr
270                275                280                285

ccg tgc gct cat gta ttg gcc atc gac ctt ctg cag aaa atg ctt gtt 913
Pro Cys Ala His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val
                290                295                300

ttt gat ccg tca aag agg att agt gcc tct gaa gca ctc cag cat cca 961
Phe Asp Pro Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro
                305                310                315

tac atg gcg cca cta tat gac ccg aat gca aac cct cct gct caa gtt 1009
Tyr Met Ala Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val
                320                325                330

cct atc gat ctc gat gta gat gag gat ttg aga gag gag atg ata aga 1057
Pro Ile Asp Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg
                335                340                345

gaa atg ata tgg aat gag atg ctt cac tac cat cca caa gct tca acc 1105
Glu Met Ile Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr
350                355                360                365

tta aac act gag ctc tga gctcaagtct tgttt 1138
Leu Asn Thr Glu Leu
                370

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&lt;210&gt; 104

&lt;211&gt; 370

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 104

Met Ala Thr Leu Val Asp Pro Pro Asn Gly Ile Arg Asn Glu Gly Lys

1	5	10	15
His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp Thr Lys Tyr	20	25	30
Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val Val Cys Ser	35	40	45
Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys Lys Ile His	50	55	60
Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu Arg Glu Leu	65	70	75
Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala Leu Lys Asp	85	90	95
Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val Tyr Leu Val	100	105	110
Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys Ser Ser Gln	115	120	125
Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln Leu Leu Arg	130	135	140
Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg Asp Leu Lys	145	150	155
Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp	165	170	175
Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe Met Thr Glu	180	185	190
Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Cys Cys	195	200	205
Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly Cys Ile Phe	210	215	220
Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr Glu Cys Leu	225	230	235
Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln Arg Glu Glu	245	250	255
Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr Ile Arg Ser	260	265	270
Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr Pro Cys Ala	275	280	285
His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val Phe Asp Pro	290	295	300
Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro Tyr Met Ala			

305                      310                      315                      320  
 Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val Pro Ile Asp  
                                  325                      330                      335  
 Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg Glu Met Ile  
                                  340                      345                      350  
 Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr Leu Asn Thr  
                                  355                      360                      365  
 Glu Leu  
                                  370

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 <211> 445  
 <212> DNA  
 <213> Arabidopsis thaliana

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                                  Met Ala Gly Lys Gly Gly Lys Gly Leu Val Ala  
                                  1                      5                      10  
 gcg aag acg atg gct gct aac aag gac aaa gac aag gac aag aag aaa 100  
 Ala Lys Thr Met Ala Ala Asn Lys Asp Lys Asp Lys Asp Lys Lys Lys  
                                  15                      20                      25  
 ccc atc tct cgc tct gct cgt gct ggt att cag ttt cca gtt gga cga 148  
 Pro Ile Ser Arg Ser Ala Arg Ala Gly Ile Gln Phe Pro Val Gly Arg  
                                  30                      35                      40  
 att cac agg caa ctg aag acc cga gtc tcg gca cat ggc aga gtt ggt 196  
 Ile His Arg Gln Leu Lys Thr Arg Val Ser Ala His Gly Arg Val Gly  
                                  45                      50                      55  
 gcc act gca gcc gtc tac aca gct tca atc ctg gag tat ctg aca gca 244  
 Ala Thr Ala Ala Val Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala  
                                  60                      65                      70                      75  
 gag gtt ctt gag ttg gct ggg aat gcg agc aag gat ctc aaa gtg aag 292  
 Glu Val Leu Glu Leu Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys  
                                  80                      85                      90  
 agg ata acg cca agg cat ctg cag ttg gcg att aga gga gat gag gag 340  
 Arg Ile Thr Pro Arg His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu  
                                  95                      100                      105  
 ctg gac aca ctc atc aag gga acg att gct gga ggt ggt gtg atc cct 388  
 Leu Asp Thr Leu Ile Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro  
                                  110                      115                      120

cac atc cac aag tct ctc atc aac aaa acc acc aag gag tga 430  
 His Ile His Lys Ser Leu Ile Asn Lys Thr Thr Lys Glu  
           125                          130                          135

tgtgtagctt tttat 445

<210> 106  
 <211> 136  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 106  
 Met Ala Gly Lys Gly Gly Lys Gly Leu Val Ala Ala Lys Thr Met Ala  
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 Ala Asn Lys Asp Lys Asp Lys Asp Lys Lys Lys Pro Ile Ser Arg Ser  
                           20                          25                          30  
 Ala Arg Ala Gly Ile Gln Phe Pro Val Gly Arg Ile His Arg Gln Leu  
           35                          40                          45  
 Lys Thr Arg Val Ser Ala His Gly Arg Val Gly Ala Thr Ala Ala Val  
       50                          55                          60  
 Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu  
       65                          70                          75                          80  
 Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg  
                           85                          90                          95  
 His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu Leu Asp Thr Leu Ile  
                           100                          105                          110  
 Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro His Ile His Lys Ser  
       115                          120                          125  
 Leu Ile Asn Lys Thr Thr Lys Glu  
       130                          135

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 <222> (14)..(916)

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                                   1                          5                          10

tat gat cca ttg cat cag aag atg tac aca ttg aat cta cct gag ctt	97
Tyr Asp Pro Leu His Gln Lys Met Tyr Thr Leu Asn Leu Pro Glu Leu	
15 20 25	
gcc aaa tct acg gtt tgt tac tca aga gat gga tgg tta cta atg cgt	145
Ala Lys Ser Thr Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg	
30 35 40	
aaa acc att tca aga gaa atg ttc ttc ttc aac ccg ttt act cgt gag	193
Lys Thr Ile Ser Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu	
45 50 55 60	
ctc ata aac gta cca aaa tgt act tta tca tat gat gcg atc gct ttc	241
Leu Ile Asn Val Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe	
65 70 75	
tct tgt gca cct aca tca ggt act tgc gtg ttg cta gca ttt aag cat	289
Ser Cys Ala Pro Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His	
80 85 90	
gtt tcg tat cgt atc acc act acg agc act tgc cat ccc aaa gca acc	337
Val Ser Tyr Arg Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr	
95 100 105	
gag tgg gtt act gag gat cta caa ttc cat cgt cgc ttc cgc agt gaa	385
Glu Trp Val Thr Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu	
110 115 120	
aca ctt aac cac agc aat gtt gtc tat gcc aaa cgt cgc ttc tat tgc	433
Thr Leu Asn His Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys	
125 130 135 140	
ctt gac ggt caa gga agc tta tat tac ttt gat ccg tct tct cga aga	481
Leu Asp Gly Gln Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg	
145 150 155	
tgg gat ttt agt tac acc tat tta ctg cca tgt cct tat atc tcg gat	529
Trp Asp Phe Ser Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp	
160 165 170	
aga ttt agt tac cag tat gag cgg aag aag aag aga att ttc ttg gct	577
Arg Phe Ser Tyr Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala	
175 180 185	
gtg cgg aaa gga gtg ttc ttt aag ata ttt aca tgt gat ggt gag aag	625
Val Arg Lys Gly Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys	
190 195 200	
ccg ata gtg cat aag tta gaa gat atc aat tgg gag gag atc aat agt	673
Pro Ile Val His Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser	
205 210 215 220	
act acg att gat gga ttg aca atc ttt acg ggt ctt tat tcc tct gag	721
Thr Thr Ile Asp Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu	
225 230 235	
gtg aga ctt aat cta cca tgg atg agg aat agt gtt tac ttt cct aga	769

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Val Arg Leu Asn Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg
      240                245                250
ctt cgt ttt aat gtc aag cgt tgt gta tca tat tcg ctt gat gaa gag 817
Leu Arg Phe Asn Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu
      255                260                265
agg tat tat ccg cgg aag cag tgg caa gaa cag gag gat tta tgt cct 865
Arg Tyr Tyr Pro Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro
      270                275                280
att gag aat ctt tgg att agg cca ccg aag aaa gct gta gat ttc atg 913
Ile Glu Asn Leu Trp Ile Arg Pro Pro Lys Lys Ala Val Asp Phe Met
      285                290                295                300
tga agataaaaagt aatg 930

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<210> 108  
 <211> 300  
 <212> PRT  
 <213> Arabidopsis thaliana

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Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg Lys Thr Ile Ser
      35                40                45
Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu Leu Ile Asn Val
      50                55                60
Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe Ser Cys Ala Pro
      65                70                75                80
Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His Val Ser Tyr Arg
      85                90                95
Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr Glu Trp Val Thr
      100                105                110
Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu Thr Leu Asn His
      115                120                125
Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys Leu Asp Gly Gln
      130                135                140
Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg Trp Asp Phe Ser
      145                150                155                160
Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp Arg Phe Ser Tyr
      165                170                175

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Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala Val Arg Lys Gly  
                     180                    185                    190  
 Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys Pro Ile Val His  
                     195                    200                    205  
 Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser Thr Thr Ile Asp  
                     210                    215                    220  
 Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu Val Arg Leu Asn  
                     225                    230                    235                    240  
 Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg Leu Arg Phe Asn  
                     245                    250                    255  
 Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu Arg Tyr Tyr Pro  
                     260                    265                    270  
 Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro Ile Glu Asn Leu  
                     275                    280                    285  
 Trp Ile Arg Pro Pro Lys Lys Ala Val Asp Phe Met  
                     290                    295                    300

<210> 109  
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gataccta	aaa	ccaaatccaa	ttca	atg	gcg	gaa	gaa	gca	aaa	tcc	aaa	gga	171			
				Met	Ala	Glu	Glu	Ala	Lys	Ser	Lys	Gly				
				1				5								
aac	gca	gct	ttc	tct	tcc	ggc	gat	tac	gcc	acc	gca	ata	acc	cat	ttc	219
Asn	Ala	Ala	Phe	Ser	Ser	Gly	Asp	Tyr	Ala	Thr	Ala	Ile	Thr	His	Phe	
10					15				20						25	
aca	gaa	gca	atc	aac	ctt	tca	cca	acc	aat	cac	atc	ctc	tac	tca	aac	267
Thr	Glu	Ala	Ile	Asn	Leu	Ser	Pro	Thr	Asn	His	Ile	Leu	Tyr	Ser	Asn	
				30					35						40	
aga	tcc	gct	tct	tac	gct	tct	ctc	cac	cgt	tac	gaa	gaa	gct	tta	tca	315
Arg	Ser	Ala	Ser	Tyr	Ala	Ser	Leu	His	Arg	Tyr	Glu	Glu	Ala	Leu	Ser	
			45					50						55		
gac	gcg	aag	aag	act	ata	gag	ctt	aaa	cct	gat	tgg	tct	aaa	gga	tat	363
Asp	Ala	Lys	Lys	Thr	Ile	Glu	Leu	Lys	Pro	Asp	Trp	Ser	Lys	Gly	Tyr	
		60					65						70			
agc	cga	tta	ggt	gct	gcg	ttt	att	gga	ttg	tcc	aag	ttt	gat	gaa	gcg	411
Ser	Arg	Leu	Gly	Ala	Ala	Phe	Ile	Gly	Leu	Ser	Lys	Phe	Asp	Glu	Ala	
	75					80						85				
gtt	gat	tcg	tat	aag	aaa	gga	tta	gag	att	gat	ccg	agt	aat	gag	atg	459
Val	Asp	Ser	Tyr	Lys	Lys	Gly	Leu	Glu	Ile	Asp	Pro	Ser	Asn	Glu	Met	
	90				95					100					105	
ctt	aaa	tcg	gga	tta	gct	gat	gct	tcg	aga	tct	agg	gtt	tcg	tca	aag	507
Leu	Lys	Ser	Gly	Leu	Ala	Asp	Ala	Ser	Arg	Ser	Arg	Val	Ser	Ser	Lys	
				110					115					120		
tcg	aat	cct	ttt	gtt	gat	gcg	ttt	caa	ggg	aag	gag	atg	tgg	gag	aag	555
Ser	Asn	Pro	Phe	Val	Asp	Ala	Phe	Gln	Gly	Lys	Glu	Met	Trp	Glu	Lys	
			125					130					135			
ttg	acg	gcg	gat	ccg	ggg	act	agg	gtt	tat	ttg	gag	cag	gat	gat	ttt	603
Leu	Thr	Ala	Asp	Pro	Gly	Thr	Arg	Val	Tyr	Leu	Glu	Gln	Asp	Asp	Phe	
		140					145					150				
gtt	aag	acg	atg	aag	gag	att	cag	agg	aac	cct	aat	aat	ctt	aat	ttg	651
Val	Lys	Thr	Met	Lys	Glu	Ile	Gln	Arg	Asn	Pro	Asn	Asn	Leu	Asn	Leu	
	155					160					165					
tat	atg	aag	gat	aag	aga	gtt	atg	aag	gct	tta	ggg	gtt	ttg	ttg	aat	699
Tyr	Met	Lys	Asp	Lys	Arg	Val	Met	Lys	Ala	Leu	Gly	Val	Leu	Leu	Asn	
	170				175					180					185	
gtg	aag	ttt	ggt	gga	tct	agt	ggt	gaa	gat	act	gag	atg	aag	gag	gct	747
Val	Lys	Phe	Gly	Gly	Ser	Ser	Gly	Glu	Asp	Thr	Glu	Met	Lys	Glu	Ala	
			190					195						200		
gat	gag	agg	aaa	gag	cct	gaa	ccg	gag	atg	gaa	cct	atg	gag	ttg	acg	795
Asp	Glu	Arg	Lys	Glu	Pro	Glu	Pro	Glu	Met	Glu	Pro	Met	Glu	Leu	Thr	
			205					210					215			
gag	gag	gag	agg	cag	aag	aag	gag	aga	aag	gag	aag	gct	ttg	aag	gag	843

Glu Glu Glu Arg Gln Lys Lys Glu Arg Lys Glu Lys Ala Leu Lys Glu  
 220 225 230

aaa ggg gaa gga aat gtt gct tat aag aag aag gat ttt ggg aga gct 891  
 Lys Gly Glu Gly Asn Val Ala Tyr Lys Lys Lys Asp Phe Gly Arg Ala  
 235 240 245

gtt gaa cat tat act aag gcc atg gag ctc gat gat gag gat att tcg 939  
 Val Glu His Tyr Thr Lys Ala Met Glu Leu Asp Asp Glu Asp Ile Ser  
 250 255 260 265

tat ttg acg aat cgt gct gct gtt tat ctt gag atg ggg aag 981  
 Tyr Leu Thr Asn Arg Ala Ala Val Tyr Leu Glu Met Gly Lys  
 270 275

gtattaagtc ttatacttgg cttaaaagtt aaaccttttag gtactttaag attaaggagg 1041  
 agatcttggg ttcttgaagt agcttatctg tttagtatag cttgtcacta gttagtacat 1101  
 ttgtgatgac cttgatgggt tttgataact ttcactctgct tcttggtgga gatttaagag 1161  
 ttttgaactt aagttttcac ttgtgctgaa agtagtttagc tttgatgag gtagaaattt 1221  
 aggggtttatg gcttcatgat ggagtttatt cacttggtct gtagaagtgg ttatctttat 1281  
 tattactgga atcaattaat cttcaagtat cctgagtggt tcaattccat tgggtctatgt 1341  
 gttcttgcac tagtcttgtt taattaacag ttggttcac tggatcttac tgtatcttgt 1401  
 gtgatgtttt acttcatttc tcaaatgaaa ttatcag tac gag gag tgc att gaa 1456  
 Tyr Glu Glu Cys Ile Glu  
 280 285

gac tgt gac aag gct gtt gaa aga ggc aga gaa ctt cgt tct gac ttc 1504  
 Asp Cys Asp Lys Ala Val Glu Arg Gly Arg Glu Leu Arg Ser Asp Phe  
 290 295 300

aag atg ata gca aga gct ctg act aga aaa gga tct gct cta gtg aaa 1552  
 Lys Met Ile Ala Arg Ala Leu Thr Arg Lys Gly Ser Ala Leu Val Lys  
 305 310 315

atg gcg aga tgc tcg aaa gac ttt gag cct gcg att gag act ttc cag 1600  
 Met Ala Arg Cys Ser Lys Asp Phe Glu Pro Ala Ile Glu Thr Phe Gln  
 320 325 330

aaa gct ctt aca gag cat cgt aat cca gat aca ttg aag aaa ctg aac 1648  
 Lys Ala Leu Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn  
 335 340 345

gat gct gag aaa gtc aag aaa gag ctg gag caa cag gag tac ttt gat 1696  
 Asp Ala Glu Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp  
 350 355 360 365

cct acg ata gcc gag gag gag cga gag aaa g gtatatatac tgatcctcag 1747  
 Pro Thr Ile Ala Glu Glu Glu Arg Glu Lys G  
 370 375



Val Gln Val Arg  
555

gaagatgttt ccaaattttc actgcgttct tttgggcttt tgttaaactg atgaaactct 2618

gatttggttt gggtcattgtt tg 2640

<210> 110

<211> 558

<212> PRT

<213> Arabidopsis thaliana

<400> 110

Met Ala Glu Glu Ala Lys Ser Lys Gly Asn Ala Ala Phe Ser Ser Gly  
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Asp Tyr Ala Thr Ala Ile Thr His Phe Thr Glu Ala Ile Asn Leu Ser  
20 25 30

Pro Thr Asn His Ile Leu Tyr Ser Asn Arg Ser Ala Ser Tyr Ala Ser  
35 40 45

Leu His Arg Tyr Glu Glu Ala Leu Ser Asp Ala Lys Lys Thr Ile Glu  
50 55 60

Leu Lys Pro Asp Trp Ser Lys Gly Tyr Ser Arg Leu Gly Ala Ala Phe  
65 70 75 80

Ile Gly Leu Ser Lys Phe Asp Glu Ala Val Asp Ser Tyr Lys Lys Gly  
85 90 95

Leu Glu Ile Asp Pro Ser Asn Glu Met Leu Lys Ser Gly Leu Ala Asp  
100 105 110

Ala Ser Arg Ser Arg Val Ser Ser Lys Ser Asn Pro Phe Val Asp Ala  
115 120 125

Phe Gln Gly Lys Glu Met Trp Glu Lys Leu Thr Ala Asp Pro Gly Thr  
130 135 140

Arg Val Tyr Leu Glu Gln Asp Asp Phe Val Lys Thr Met Lys Glu Ile  
145 150 155 160

Gln Arg Asn Pro Asn Asn Leu Asn Leu Tyr Met Lys Asp Lys Arg Val  
165 170 175

Met Lys Ala Leu Gly Val Leu Leu Asn Val Lys Phe Gly Gly Ser Ser  
180 185 190

Gly Glu Asp Thr Glu Met Lys Glu Ala Asp Glu Arg Lys Glu Pro Glu  
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Glu Arg Lys Glu Lys Ala Leu Lys Glu Lys Gly Glu Gly Asn Val Ala

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Cys Ser Lys Asp Phe Glu Pro Ala Ile Glu Thr Phe Gln Lys Ala Leu						
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Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn Asp Ala Glu						
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206

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Met Phe Gly Ser Ser Pro Trp Pro Leu Leu Pro Gln Leu Pro Pro Pro
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Tyr Gln Thr Thr Pro Ser Cys Asn Leu Glu Gln Lys Pro Leu Ile Thr
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Thr	Trp	Ser	Thr	Gln	Phe	Glu	Asn	Phe	Leu	Ala	Thr	Lys	Trp	Thr	Thr		
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Pro	Val	Asp	Glu	Val	Gly	Leu	Tyr	Thr	Gly	Thr	Gly	Asp	Val	Lys	Tyr		
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Lys Ala Glu Ser Ala Ala Pro Val Pro Arg Pro Val Pro Leu Ser Lys
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Leu Gln Arg Ala Trp Glu Ala Asp Pro Asn Ser Val Asp Glu Ser Trp
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Ile Ser Gly Gln Thr Ile Gln Glu Ser Met Arg Leu Leu Leu Leu Val
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Gly Leu Glu Lys Arg Glu Ile Pro Glu Asp Leu Thr Pro Gly Leu Tyr  
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 Gly Phe Thr Glu Ala Asp Leu Asp Arg Glu Phe Phe Leu Gly Val Trp  
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 Arg Met Ser Gly Phe Leu Ser Glu Asn Arg Pro Val Gln Thr Leu Arg  
 180 185 190  
 Ser Ile Leu Ser Arg Leu Glu Gln Ala Tyr Cys Gly Thr Ile Gly Tyr  
 195 200 205  
 Glu Tyr Met His Ile Ala Asp Arg Asp Lys Cys Asn Trp Leu Arg Asp  
 210 215 220  
 Lys Ile Glu Thr Pro Thr Pro Arg Gln Tyr Asn Ser Glu Arg Arg Met  
 225 230 235 240  
 Val Ile Tyr Asp Arg Leu Thr Trp Ser Thr Gln Phe Glu Asn Phe Leu  
 245 250 255  
 Ala Thr Lys Trp Thr Thr Ala Lys Arg Phe Gly Leu Glu Gly Ala Glu  
 260 265 270  
 Ser Leu Ile Pro Gly Met Lys Glu Met Phe Asp Arg Ser Ala Asp Leu  
 275 280 285  
 Gly Val Glu Asn Ile Val Ile Gly Met Pro His Arg Gly Arg Leu Asn  
 290 295 300  
 Val Leu Gly Asn Val Val Arg Lys Pro Leu Arg Gln Ile Phe Ser Glu  
 305 310 315 320  
 Phe Ser Gly Gly Thr Arg Pro Val Asp Glu Val Gly Leu Tyr Thr Gly  
 325 330 335  
 Thr Gly Asp Val Lys Tyr His Leu Gly Thr Ser Tyr Asp Arg Pro Thr  
 340 345 350  
 Arg Gly Gly Lys His Leu His Leu Ser Leu Val Ala Asn Pro Ser His  
 355 360 365  
 Leu Glu Ala Val Asp Pro Val Val Ile Gly Lys Thr Arg Ala Lys Gln  
 370 375 380  
 Tyr Tyr Thr Lys Asp Glu Asn Arg Thr Lys Asn Met Gly Ile Leu Ile  
 385 390 395 400  
 His Gly Asp Gly Ser Phe Ala Gly Gln Gly Val Val Tyr Glu Thr Leu  
 405 410 415  
 His Leu Ser Ala Leu Pro Asn Tyr Cys Thr Gly Gly Thr Val His Ile  
 420 425 430  
 Val Val Asn Asn Gln Val Ala Phe Thr Thr Asp Pro Arg Glu Gly Arg  
 435 440 445

Ser Ser Gln Tyr Cys Thr Asp Val Ala Lys Ala Leu Ser Ala Pro Ile  
 450 455 460  
 Phe His Val Asn Ala Asp Asp Ile Glu Ala Val Val His Ala Cys Glu  
 465 470 475 480  
 Leu Ala Ala Glu Trp Arg Gln Thr Phe His Ser Asp Val Val Val Asp  
 485 490 495  
 Leu Val Cys Tyr Arg Arg Phe Gly His Asn Glu Ile Asp Glu Pro Ser  
 500 505 510  
 Phe Thr Gln Pro Lys Met Tyr Lys Val Ile Arg Ser His Pro Ser Ser  
 515 520 525  
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 Glu Tyr Glu Ala Ser Lys Asp Tyr Ile Pro Gln Lys Arg Asp Trp Leu  
 565 570 575  
 Ala Ser His Trp Thr Gly Phe Lys Ser Pro Glu Gln Ile Ser Arg Ile  
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 Arg Asn Thr Gly Val Lys Pro Glu Ile Leu Lys Asn Val Gly Lys Ala  
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 Ile Ser Thr Phe Pro Glu Asn Phe Lys Pro His Arg Gly Val Lys Arg  
 610 615 620  
 Val Tyr Glu Gln Arg Ala Gln Met Ile Glu Ser Gly Glu Gly Ile Asp  
 625 630 635 640  
 Trp Gly Leu Gly Glu Ala Leu Ala Phe Ala Thr Leu Val Val Glu Gly  
 645 650 655  
 Asn His Val Arg Leu Ser Gly Gln Asp Val Glu Arg Gly Thr Phe Ser  
 660 665 670  
 His Arg His Ser Val Leu His Asp Gln Glu Thr Gly Glu Glu Tyr Cys  
 675 680 685  
 Pro Leu Asp His Leu Ile Lys Asn Gln Asp Pro Glu Met Phe Thr Val  
 690 695 700  
 Ser Asn Ser Ser Leu Ser Glu Phe Gly Val Leu Gly Phe Glu Leu  
 705 710 715 720  
 Gly Tyr Ser Met Glu Asn Pro Asn Ser Leu Val Ile Trp Glu Ala Gln  
 725 730 735  
 Phe Gly Ap Phe Ala Asn Gly Ala Gln Val Met Phe Asp Gln Phe Ile  
 740 745 750

Ser Ser Gy Glu Ala Lys Trp Leu Arg Gln Thr Gly Leu Val Val Leu  
                             755                            760                            765  
 Leu Pro Hs Gly Tyr Asp Gly Gln Gly Pro Glu His Ser Ser Gly Arg  
                             770                            775                            780  
 Leu Glu Ag Phe Leu Gln Met Ser Asp Asp Asn Pro Tyr Val Ile Pro  
                             785                            790                            795  
 Glu Met Asp Pro Thr Leu Arg Lys Gln Ile Gln Glu Cys Asn Trp Gln  
                             800                            805                            810  
 Val Val Asn Val Thr Thr Pro Ala Asn Trp Phe His Val Leu Arg Arg  
                             815                            820                            825  
 Gln Ile His Arg Asp Phe Arg Lys Pro Leu Ile Val Met Ala Pro Lys  
                             830                            835                            840  
 Asn Leu Leu Arg His Lys Gln Cys Val Ser Asn Leu Ser Glu Phe Asp  
                             845                            850                            855  
 Asp Val Lys Gly His Pro Gly Phe Asp Lys Gln Gly Thr Arg Phe Lys  
                             860                            865                            870  
 Arg Leu Ile Lys Asp Gln Ser Gly His Ser Asp Leu Glu Glu  
                             875                            880                            885  
 Asp Ala Glu Ile Val Trp Cys Gln Glu Glu Pro Met Asn Met Gly Gly  
                             890                            895                            900  
 Tyr Gln Tyr Ile Ala Leu Arg Leu Cys Thr Ala Met Lys Ala Leu Gln  
                             905                            910                            915  
 Arg Gly Asn Phe Asn Asp Ile Lys Tyr Val Gly Arg Leu Pro Ser Ala  
                             920                            925                            930  
 Ala Thr Ala Thr Gly Phe Tyr Gln Leu His Val Lys Glu Gln Thr Asp  
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&lt;222&gt; (465)..(662)

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&lt;222&gt; (783)..(1166)

&lt;400&gt; 115

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tgcattttta ctctcttgac gcta atg ttc att cgg gtt tcc gct cga ccc      51
                               Met Phe Ile Arg Val Ser Ala Arg Pro
                               1           5

gcg aca ttc gtc gag gat ttc aaa gcc gcc tgg tcg gaa tct cac atc      99
Ala Thr Phe Val Glu Asp Phe Lys Ala Ala Trp Ser Glu Ser His Ile
 10           15           20           25

cgt caa atg gaa gac gga aaa gct atc cag ctc gtc ctt gat cag agc      147
Arg Gln Met Glu Asp Gly Lys Ala Ile Gln Leu Val Leu Asp Gln Ser
           30           35           40

act g gtacaccaac gccacagtta tatttttaaa cggaacatt ttgaaattaa      201
Thr G

tggtgttttt atgtaatata ctctcactgt acatgttcat atttgtcttt taaag ga      258
                               ly

tgt gga ttt gct tcc aaa aga aaa tat cta ttc gga cga gtg agc atg      306
Cys Gly Phe Ala Ser Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met
 45           50           55

aag atc aaa ctc att ccc gga gac tct gcc ggt acg gtc acc gct ttc      354
Lys Ile Lys Leu Ile Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe
 60           65           70           75

tac gtaagtctat cattttactc cactagtttt gaaattttac acattcacac      407
Tyr

aataaaaaat aacattttct tgaaacacta acggtcaaat cattgatatg tctatag      464

atg aac tcc gat acg gcc acg gtg aga gac gag cta gat ttt gag ttc      512
Met Asn Ser Asp Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe
 80           85           90

ttg gga aac aga agt ggt caa cct tac tca gtg caa aca aac ata ttt      560
Leu Gly Asn Arg Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe
 95           100          105

gct cat ggc aaa gga gat aga gaa caa aga gtt aat ctt tgg ttc gac      608
Ala His Gly Lys Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp
 110          115          120

cca tct atg gat tac cac act tac act atc tta tgg tca cac aaa cac      656
Pro Ser Met Asp Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His
125          130          135          140

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att gtg taagcttttc tctaattgta ctttcaacta gaatcaacat ttactgtttc 712  
Ile Val

aaaacaaaaa atcaccattt actgttttaa aaaaccttag tttaacgtgg gggtgttttg 772

gttactcagt ttt tac gta gac gat gtg cca ata aga gaa tac aaa aac 821  
Phe Tyr Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn  
145 150 155

aac gaa gcc aag aac ata gct tac cca aca tca caa cct atg gga gta 869  
Asn Glu Ala Lys Asn Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val  
160 165 170

tac tca aca tta tgg gaa gca gat gac tgg gca aca cgt ggt gga tta 917  
Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu  
175 180 185

gag aaa att gat tgg agc aaa gct cca ttt tat gct tat tac aaa gat 965  
Glu Lys Ile Asp Trp Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp  
190 195 200

ttc gac atc gaa ggt tgt cct gtt cct gga cca acc ttt tgt cca tcg 1013  
Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser  
205 210 215

aac cct cat aat tgg tgg gaa ggt tat gcc tat cag tct ctt aac gcc 1061  
Asn Pro His Asn Trp Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala  
220 225 230 235

gtt gaa gct cga cgt tac cgg tgg gtt aga gta aac cat atg gtt tat 1109  
Val Glu Ala Arg Arg Tyr Arg Trp Val Arg Val Asn His Met Val Tyr  
240 245 250

gat tat tgt act gac cgg tct agg ttt cct gtc cca cca ccc gag tgt 1157  
Asp Tyr Cys Thr Asp Arg Ser Arg Phe Pro Val Pro Pro Pro Glu Cys  
255 260 265

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Arg Ala  
270

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Ala Ile Gln Leu Val Leu Asp Gln Ser Thr Gly Cys Gly Phe Ala Ser  
35 40 45

Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met Lys Ile Lys Leu Ile  
     50                    55                    60  
 Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe Tyr Met Asn Ser Asp  
     65                    70                    75                    80  
 Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe Leu Gly Asn Arg  
                     85                    90                    95  
 Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe Ala His Gly Lys  
                     100                    105                    110  
 Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp Pro Ser Met Asp  
                     115                    120                    125  
 Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His Ile Val Phe Tyr  
     130                    135                    140  
 Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn Asn Glu Ala Lys Asn  
     145                    150                    155                    160  
 Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val Tyr Ser Thr Leu Trp  
                     165                    170                    175  
 Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu Glu Lys Ile Asp Trp  
                     180                    185                    190  
 Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp Phe Asp Ile Glu Gly  
                     195                    200                    205  
 Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser Asn Pro His Asn Trp  
     210                    215                    220  
 Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala Val Glu Ala Arg Arg  
     225                    230                    235                    240  
 Tyr Arg Trp Val Arg Val Asn His Met Val Tyr Asp Tyr Cys Thr Asp  
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 Arg Ser Arg Phe Pro Val Pro Pro Pro Glu Cys Arg Ala  
                     260                    265

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                               1           5

atc cgc aga acc cta acc aaa cca cac gcc act ttt tcc cgg tgt cgc 99
Ile Arg Arg Thr Leu Thr Lys Pro His Gly Thr Phe Ser Arg Cys Arg
10           15           20           25

tac tta tca acc gcc gct gct gcg acg gag gtg aat tac gag gat gaa 147
Tyr Leu Ser Thr Ala Ala Ala Ala Thr Glu Val Asn Tyr Glu Asp Glu
30           35           40

tcg att atg atg aaa gga gtt cga att tca ggt aga cct ctt tac tta 195
Ser Ile Met Met Lys Gly Val Arg Ile Ser Gly Arg Pro Leu Tyr Leu
45           50           55

gat atg caa gcg acg act ccg att gat cct aga gta ttc gat gcg atg 243
Asp Met Gln Ala Thr Thr Pro Ile Asp Pro Arg Val Phe Asp Ala Met
60           65           70

aat gct tca cag atc cat gag tat ggg aat cct cac tcg cga acg cat 291
Asn Ala Ser Gln Ile His Glu Tyr Gly Asn Pro His Ser Arg Thr His
75           80           85

ctc tac gcc tgg gaa gct gag aac gcc gtc gag aac gca cga aac cag 339
Leu Tyr Gly Trp Glu Ala Glu Asn Ala Val Glu Asn Ala Arg Asn Gln
90           95           100           105

gtc gcg aaa ctg atc gaa gct tca ccg aag gag atc gta ttc gtg tcc 387
Val Ala Lys Leu Ile Glu Ala Ser Pro Lys Glu Ile Val Phe Val Ser
110           115           120

ggg gca acg gag gcg aac aat atg gcg gtg aaa gga gtg atg cac ttt 435
Gly Ala Thr Glu Ala Asn Asn Met Ala Val Lys Gly Val Met His Phe
125           130           135

tac aag gac acg aag aaa cat gtg ata act aca cag act gag cat aag 483
Tyr Lys Asp Thr Lys Lys His Val Ile Thr Thr Gln Thr Glu His Lys
140           145           150

tgt gtg ctt gat tcg tgt agg cat ttg cag caa gaa gga ttt gag gta 531
Cys Val Leu Asp Ser Cys Arg His Leu Gln Gln Glu Gly Phe Glu Val
155           160           165

act tat tta cct gtg aaa act gat gga ttg gtt gat tta gag atg ttg 579
Thr Tyr Leu Pro Val Lys Thr Asp Gly Leu Val Asp Leu Glu Met Leu
170           175           180           185

aga gaa gct att agg cca gac aca ggg cta gtt tct att atg gct gtg 627
Arg Glu Ala Ile Arg Pro Asp Thr Gly Leu Val Ser Ile Met Ala Val
190           195           200

aac aat gag att ggt gtg gtt caa cct atg gag gag att ggt atg att 675
Asn Asn Glu Ile Gly Val Val Gln Pro Met Glu Glu Ile Gly Met Ile
205           210           215

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tgc aaa gag cat aat gtt ccg ttt cat act gat gct gct caa gct att	723
Cys Lys Glu His Asn Val Pro Phe His Thr Asp Ala Ala Gln Ala Ile	
220 225 230	
ggg aag ata cct gtt gat gtt aag aag tgg aat gtt gct ttg atg tct	771
Gly Lys Ile Pro Val Asp Val Lys Lys Trp Asn Val Ala Leu Met Ser	
235 240 245	
atg agt gct cac aag atc tat gga ccg aaa ggt gtt ggt gct ttg tat	819
Met Ser Ala His Lys Ile Tyr Gly Pro Lys Gly Val Gly Ala Leu Tyr	
250 255 260 265	
gtg agg agg agg ccg aga atc agg ctt gag ccg ttg atg aat ggt gga	867
Val Arg Arg Arg Pro Arg Ile Arg Leu Glu Pro Leu Met Asn Gly Gly	
270 275 280	
ggt cag gag agg gga ttg cgt agt ggt acg ggg gct acg cag cag att	915
Gly Gln Glu Arg Gly Leu Arg Ser Gly Thr Gly Ala Thr Gln Gln Ile	
285 290 295	
gtt ggg ttc ggg gct gct tgt gag ttg gct atg aag gag atg gag tat	963
Val Gly Phe Gly Ala Ala Cys Glu Leu Ala Met Lys Glu Met Glu Tyr	
300 305 310	
gat gag aag tgg att aag ggg tta cag gag agg ttg ctg aat ggg gtt	1011
Asp Glu Lys Trp Ile Lys Gly Leu Gln Glu Arg Leu Leu Asn Gly Val	
315 320 325	
aga gag aag ctt gat ggt gtt gtg gtg aat ggt tca atg gat agt cga	1059
Arg Glu Lys Leu Asp Gly Val Val Val Asn Gly Ser Met Asp Ser Arg	
330 335 340 345	
tat gta ggg aat ttg aat ttg tcg ttt gct tat gtt gaa gga gag agt	1107
Tyr Val Gly Asn Leu Asn Leu Ser Phe Ala Tyr Val Glu Gly Glu Ser	
350 355 360	
ttg ttg atg gga ttg aag gaa gtt gca gtg tct agt gga agt gct tgt	1155
Leu Leu Met Gly Leu Lys Glu Val Ala Val Ser Ser Gly Ser Ala Cys	
365 370 375	
act agt gcg agt ttg gag cct tct tat gtg ttg aga gct ttg ggt gtg	1203
Thr Ser Ala Ser Leu Glu Pro Ser Tyr Val Leu Arg Ala Leu Gly Val	
380 385 390	
gat gaa gac atg gct cac act tcg att agg ttt ggg att ggt agg ttt	1251
Asp Glu Asp Met Ala His Thr Ser Ile Arg Phe Gly Ile Gly Arg Phe	
395 400 405	
acc acg aag gaa gag att gat aaa gcg gtc gag ctt acg gtt aaa caa	1299
Thr Thr Lys Glu Glu Ile Asp Lys Ala Val Glu Leu Thr Val Lys Gln	
410 415 420 425	
gtt gag aag ttg agg gaa atg agc ccg ctt tat gaa atg gtt aaa gaa	1347
Val Glu Lys Leu Arg Glu Met Ser Pro Leu Tyr Glu Met Val Lys Glu	
430 435 440	
ggg atc gat atc aag aac att caa tgg tct caa cac tga ttcaacagtt	1396

Gly Ile Asp Ile Lys Asn Ile Gln Trp Ser Gln His  
 445 450

cca

1399

&lt;210&gt; 118

&lt;211&gt; 453

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 118

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Pro His Gly Thr Phe Ser Arg Cys Arg Tyr Leu Ser Thr Ala Ala Ala  
 20 25 30

Ala Thr Glu Val Asn Tyr Glu Asp Glu Ser Ile Met Met Lys Gly Val  
 35 40 45

Arg Ile Ser Gly Arg Pro Leu Tyr Leu Asp Met Gln Ala Thr Thr Pro  
 50 55 60

Ile Asp Pro Arg Val Phe Asp Ala Met Asn Ala Ser Gln Ile His Glu  
 65 70 75 80

Tyr Gly Asn Pro His Ser Arg Thr His Leu Tyr Gly Trp Glu Ala Glu  
 85 90 95

Asn Ala Val Glu Asn Ala Arg Asn Gln Val Ala Lys Leu Ile Glu Ala  
 100 105 110

Ser Pro Lys Glu Ile Val Phe Val Ser Gly Ala Thr Glu Ala Asn Asn  
 115 120 125

Met Ala Val Lys Gly Val Met His Phe Tyr Lys Asp Thr Lys Lys His  
 130 135 140

Val Ile Thr Thr Gln Thr Glu His Lys Cys Val Leu Asp Ser Cys Arg  
 145 150 155 160

His Leu Gln Gln Glu Gly Phe Glu Val Thr Tyr Leu Pro Val Lys Thr  
 165 170 175

Asp Gly Leu Val Asp Leu Glu Met Leu Arg Glu Ala Ile Arg Pro Asp  
 180 185 190

Thr Gly Leu Val Ser Ile Met Ala Val Asn Asn Glu Ile Gly Val Val  
 195 200 205

Gln Pro Met Glu Glu Ile Gly Met Ile Cys Lys Glu His Asn Val Pro  
 210 215 220

Phe His Thr Asp Ala Ala Gln Ala Ile Gly Lys Ile Pro Val Asp Val  
 225 230 235 240

Lys	Lys	Trp	Asn	Val	Ala	Leu	Met	Ser	Met	Ser	Ala	His	Lys	Ile	Tyr	
				245					250					255		
Gly	Pro	Lys	Gly	Val	Gly	Ala	Leu	Tyr	Val	Arg	Arg	Arg	Pro	Arg	Ile	
				260					265					270		
Arg	Leu	Glu	Pro	Leu	Met	Asn	Gly	Gly	Gly	Gln	Glu	Arg	Gly	Leu	Arg	
				275					280					285		
Ser	Gly	Thr	Gly	Ala	Thr	Gln	Gln	Ile	Val	Gly	Phe	Gly	Ala	Ala	Cys	
				290					295					300		
Glu	Leu	Ala	Met	Lys	Glu	Met	Glu	Tyr	Asp	Glu	Lys	Trp	Ile	Lys	Gly	
				305					310					315		
Leu	Gln	Glu	Arg	Leu	Leu	Asn	Gly	Val	Arg	Glu	Lys	Leu	Asp	Gly	Val	
				325					330					335		
Val	Val	Asn	Gly	Ser	Met	Asp	Ser	Arg	Tyr	Val	Gly	Asn	Leu	Asn	Leu	
				340					345					350		
Ser	Phe	Ala	Tyr	Val	Glu	Gly	Glu	Ser	Leu	Leu	Met	Gly	Leu	Lys	Glu	
				355					360					365		
Val	Ala	Val	Ser	Ser	Gly	Ser	Ala	Cys	Thr	Ser	Ala	Ser	Leu	Glu	Pro	
				370					375					380		
Ser	Tyr	Val	Leu	Arg	Ala	Leu	Gly	Val	Asp	Glu	Asp	Met	Ala	His	Thr	
				385					390					395		
Ser	Ile	Arg	Phe	Gly	Ile	Gly	Arg	Phe	Thr	Thr	Lys	Glu	Glu	Ile	Asp	
				405					410					415		
Lys	Ala	Val	Glu	Leu	Thr	Val	Lys	Gln	Val	Glu	Lys	Leu	Arg	Glu	Met	
				420					425					430		
Ser	Pro	Leu	Tyr	Glu	Met	Val	Lys	Glu	Gly	Ile	Asp	Ile	Lys	Asn	Ile	
				435					440					445		
Gln	Trp	Ser	Gln	His												
				450												

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&lt;221&gt; CDS

&lt;222&gt; (2697)..(3076)

&lt;400&gt; 119

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        1              5              10

ctt ctt tct tgt ttt ctc caa gtt tct tcc aat gga gac gct gag ata 97
Leu Leu Ser Cys Phe Leu Gln Val Ser Ser Asn Gly Asp Ala Glu Ile
  15              20              25              30

ttg agt aga gtt aaa aag acc cga ctt ttc gac ccc gat gga aat tta 145
Leu Ser Arg Val Lys Lys Thr Arg Leu Phe Asp Pro Asp Gly Asn Leu
              35              40              45

caa gat tgg gtc ata acc gga gat aat cgg agt cca tgt aat tgg acg 193
Gln Asp Trp Val Ile Thr Gly Asp Asn Arg Ser Pro Cys Asn Trp Thr
              50              55              60

gga atc aca tgc cac atc aga aaa ggt agc tcc ctc gcc gtc act acc 241
Gly Ile Thr Cys His Ile Arg Lys Gly Ser Ser Leu Ala Val Thr Thr
        65              70              75

att gat ctc tcc ggc tat aat atc tcc ggt ggc ttt ccc tac gga ttc 289
Ile Asp Leu Ser Gly Tyr Asn Ile Ser Gly Gly Phe Pro Tyr Gly Phe
      80              85              90

tgt cgt atc cgt aca ctc atc aac atc act ctt tct caa aac aat ctc 337
Cys Arg Ile Arg Thr Leu Ile Asn Ile Thr Leu Ser Gln Asn Asn Leu
      95              100              105              110

aat ggt acg att gat tct gct cct ctc tcc ctc tgt tct aaa ctt cag 385
Asn Gly Thr Ile Asp Ser Ala Pro Leu Ser Leu Cys Ser Lys Leu Gln
              115              120              125

aat ttg att ctc aat caa aac aac ttc tcc ggt aaa tta ccg gaa ttc 433
Asn Leu Ile Leu Asn Gln Asn Asn Phe Ser Gly Lys Leu Pro Glu Phe
              130              135              140

tca ccg gag ttt cgt aaa tta cga gtc ctc gaa ttg gaa tca aac ctc 481
Ser Pro Glu Phe Arg Lys Leu Arg Val Leu Glu Leu Glu Ser Asn Leu
              145              150              155

ttc acc ggt gag att cct caa agt tac ggg aga ctc act gct ctg caa 529
Phe Thr Gly Glu Ile Pro Gln Ser Tyr Gly Arg Leu Thr Ala Leu Gln
        160              165              170

gtt ctg aat ctt aat ggt aac ccg ctc agt gga atc gtt ccg gcg ttt 577
Val Leu Asn Leu Asn Gly Asn Pro Leu Ser Gly Ile Val Pro Ala Phe
      175              180              185              190

ttg ggt tat ctg act gag tta act cgt ctt gat ctc gct tac atc agt 625
Leu Gly Tyr Leu Thr Glu Leu Thr Arg Leu Asp Leu Ala Tyr Ile Ser
              195              200              205

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ttt gat cct agt ccg att cca tca acc ttg ggg aac ttg tgc aat ctg	673
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210 215 220	
act gat ctt cgg cta act cac tgc aac ctc gtc gga gaa att cct gat	721
Thr Asp Leu Arg Leu Thr His Ser Asn Leu Val Gly Glu Ile Pro Asp	
225 230 235	
tcg atc atg aat ctg gtg ttg tta gag aat ctt gat tta gct atg aat	769
Ser Ile Met Asn Leu Val Leu Leu Glu Asn Leu Asp Leu Ala Met Asn	
240 245 250	
agt ctc acc gga gaa ata cct gag agt atc gga aga ctc gaa tcg gtt	817
Ser Leu Thr Gly Glu Ile Pro Glu Ser Ile Gly Arg Leu Glu Ser Val	
255 260 265 270	
tac cag att gag ctc tac gat aac cgg tta tct gga aaa tta ccg gag	865
Tyr Gln Ile Glu Leu Tyr Asp Asn Arg Leu Ser Gly Lys Leu Pro Glu	
275 280 285	
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Leu Cys Tyr Arg Arg Lys Leu Gln Lys Ile Ile Thr Phe Ser Asn Gln	
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Gln Leu Glu Ile Ser Ala Asn Asn Phe Ser Gly Val Ile Pro Val Lys	
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